

SEQUENCE LISTING

<110> PE CORPORATION (NY);
THE THIRD INSITITUTE OF OCEANOGRAPHY, STATE OCEANIC ADMINISTRATION,
CHINA ;
SINOGENOMAX CO. LTD.

<120> PRIMARY NUCLEOTIDE SEQUENCE OF THE
SHRIMP WHITE SPOT BACILLIFORM VIRUS (WSBV), DISCOVERY
SYSTEMS CONTAINING THIS SEQUENCE AND DETECTION KITS AND
ANTIVIRAL TARGETS FOR DETECTION AND CONTROLLING SHRIMP VIRUS
OUTBREAK AND SPREAD

<130> CL000895-PCT

<150> 99124717.5

<151> 1999-11-24

<160> 293

<170> FastSEQ for Windows Version 4.0

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<211> 305107

<212> DNA

<213> SHRIMP

<400> 1

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88

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Lys	Asp	Leu	Thr	Val	His	Ala	Asn	Ser	Asp	Thr	Tyr	Leu	Thr	Phe	Pro
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 65          70          75          80
Val Lys Pro Ala Ala Lys Ser Leu Asn Thr Asn Met Val Asn Arg Ile
 85          90          95
Lys Ile Ile Ala Val Glu Asp Thr Ser Pro Arg Ser Met Val Asn Glu
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Asp Lys Leu Gly Gly Ile Tyr Tyr Ala Asn Phe Asn Glu Leu Glu Thr
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90

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Thr	Tyr	Ala	Ile	Asn	Trp	Arg	Arg	Asp	Phe	Phe	Cys	Ser	Lys	Gly	Phe	
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 Asn Lys Val Thr Lys Glu Asp Ile Asp Ser Cys Leu Pro Ser Trp Leu
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Asn	Lys	Tyr	Met	Asp	Val	Val	Cys	Lys	Ser	Met	Gln	His	Asn	Leu	Arg	
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1685					1690					1695						
His	Gly	Ser	Ile	Val	Thr	Ser	Thr	Cys	Thr	Ala	Gln	Glu	Lys	Gly	Glu	
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1730					1735					1740						
Ser	Gly	Val	Ser	Glu	Phe	Pro	Ile	Lys	Asp	Lys	Ser	Ile	Ser	Asn	Pro	
1745					1750					1755					1760	
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1765					1770					1775						
Ser	Pro	Thr	Asn	Asn	Leu	His	Phe	Ser	Met	Ser	Glu	Asp	Val	Leu	Phe	
1780					1785					1790						
Cys	Gly	Gln	Val	His	Pro	Met	Lys	Arg	Val	Gln	Phe	Ser	Leu	His	Val	
1795					1800					1805						
Lys	Arg	Thr	Gly	Gly	Ala	Leu	Lys	Ser	Thr	Phe	Glu	Glu	Glu	Glu	Gly	
1810					1815					1820						
Leu	Pro	Thr	Lys	Ile	Phe	Ser	Pro	Asn	Phe	Ala	Thr	Tyr	Pro	Leu	Phe	
1825					1830					1835					1840	
Lys	Lys	Cys	Lys	Met	Tyr	Gly	Ala	Ile	Ile	Ile	Ala	Met	Thr	Glu	Met	
1845					1850					1855						
Gln	Gly	His	Glu	Phe	Ala	Lys	Tyr	Ser	Thr	Leu	Asp	Ile	Arg	Lys	Ser	
1860					1865					1870						
Met	Phe	Thr	Gly	Val	Gly	Thr	Val	Val	Asp	Leu	Glu	Lys	Ile	Ser	Gly	
1875					1880					1885						

Glu Gly Asn Glu Val Met Asp Lys Val Asp Lys Phe Ile Val Lys Asn
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 Val Ser Cys Ala Ile His
 1925

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 <213> SHRIMP

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 ttccctgatc cgaaatcggc attaaactttt tttgtaccga acaagagcct caatgcgttt 240
 gcatgggacg tactaaaaac gccagctagc gttgaaattg atatagggaa gagaattcct 300
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 aaggatatcg caattaagcc tgaaaaaaga ggttcatctg ctgtatggga tgaagtatat 660
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 35 40 45
 Ile Ser Ala Trp Val Thr Glu Val Ala Ala Asp Val Phe Pro Asp Pro
 50 55 60
 Lys Ser Ala Leu Thr Phe Val Pro Asn Lys Ser Leu Asn Ala Phe
 65 70 75 80
 Ala Trp Asp Val Leu Lys Thr Pro Ala Ser Val Glu Ile Asp Ile Gly
 85 90 95
 Lys Arg Ile Pro Gln Leu Ile Glu Asn Leu His Met Ser Asp Phe Thr
 100 105 110
 Val Ala Ile Phe Arg Val Lys Cys Asp Asp Gln Gly Arg Tyr Glu Thr
 115 120 125
 Ser Tyr Asn Leu Ser Pro Ser Met Gly Gly Lys Ile Asn His Gly Leu
 130 135 140
 Ile Arg Thr Leu Ala Lys Ala Gln Asp Ile Val Val Trp Lys Arg Asp
 145 150 155 160
 Phe Ser Leu Thr Ile Glu Asn Phe Glu Val Asp Asn Gly Lys Lys Arg
 165 170 175
 Leu Asp Phe Leu Phe Asn Asn Gln Thr Asp Lys Ser Cys Phe Val Lys
 180 185 190
 Ile Phe His Glu Met Glu Ser Glu Lys Asp Ile Ala Ile Lys Pro Glu
 195 200 205
 Lys Arg Gly Ser Ser Ala Val Trp Asp Glu Val Tyr Ser Asp Ile Val

210		215		220
Thr Lys Asn Thr Arg Asn Ala Lys Phe Ser Leu	Arg Tyr Arg Asn Glu			
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 tctctcctgg cgggcacagc actggccggc acgatcgctt ctgcgctggg atcaatacca 180
 ggagtgggcg gtgcattcaa gaaagccttt ggaaaaggaa aggggaaagg aggacaaaaa 240
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 35 40 45
 Ala Ser Ala Leu Gly Ser Ile Pro Gly Val Gly Gly Ala Phe Lys Lys
 50 55 60
 Ala Phe Gly Lys Gly Lys Gly Lys Gly Gly Pro Lys Thr Pro Asp Gly
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 <212> DNA
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 gaacaagaag aactggtaga ggactcgtca agtaacaagc gccccagaat taaggaagag 180
 aaggaggaag aacacaaaaga aacacatcac ctctccctcc catgtaaaga agaagaagac 240
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WO 01/38351

PCT/US00/28888

101

<210> 19
 <211> 228
 <212> PRT
 <213> SHRIMP

<400> 19

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Lys	Val	Lys	Val	Glu	Val	Lys	Met	Glu	Gln	Glu	Glu	Leu	Val	Glu	Asp
		35					40					45			
Ser	Ser	Ser	Asn	Lys	Arg	Pro	Arg	Ile	Lys	Glu	Glu	Lys	Glu	Glu	Glu
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His	Lys	Glu	Thr	His	His	Leu	Ser	Leu	Pro	Cys	Lys	Glu	Glu	Glu	Asp
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Asp	Gly	Glu	Glu	Glu	Glu	Tyr	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Tyr
				85					90					95	
Glu	Asp	Arg	Val	Asp	Asp	Asp	Thr	Ala	Glu	Lys	Met	Glu	Asn	Leu	Leu
			100					105					110		
Val	Gln	Leu	Asp	Asn	Thr	Thr	Lys	Asn	Ile	Lys	Leu	Lys	Asn	Pro	Leu
		115					120					125			
Arg	Glu	His	Asp	Met	Ala	Val	Ser	His	Tyr	Glu	His	Glu	Phe	Glu	Val
		130				135					140				
Gln	Asn	Thr	Val	Asn	Phe	Ser	Phe	Gly	Val	Leu	Ser	Asp	Ile	Gly	Phe
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Leu	Ile	Asn	Arg	Glu	Ala	Val	Ser	Arg	Trp	Gly	Asn	Thr	Pro	Pro	Pro
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Lys	Glu	Phe	Gly	Asp	Met	Glu	Ile	Gly	Ser	Leu	Thr	Val	Asn	Gln	Leu
			180					185					190		
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		195					200					205			
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225															

<210> 20
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 <212> DNA
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 <212> PRT
 <213> SHRIMP

<400> 21

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			20					25					30		
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		35					40					45			
Leu	Ser	Phe	Lys	Ser	Val	Asp	Arg	Val	Thr	Lys	Ser	Glu	Leu	Arg	Asp
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Gly	Ile	Val	Arg	Leu	Lys	Asp	Lys	Glu	Val	Leu	His	Ile	Lys	Asn	Gly
65					70				75					80	
Val	His	Arg	Leu	Arg	Gln	Leu	Thr	Gly	Asp	Asn	Thr	Leu	Gln	Val	Gly
			85					90					95		
Leu	Lys	Tyr	Thr	His	Asn	Leu	Pro	Arg	Leu	Gly	Ser	Leu	Leu	Gln	Asp
		100					105					110			
Asp	Gly	Cys	Glu	Asp	Tyr	Gly	Glu	Lys	Trp	Asn	Glu	Ser	Leu	Pro	Ile
	115					120					125				
Asp	Met	Gln	Asn	Ile	Asn	Lys	Ile	Val	Lys	Glu	Lys	Ala	Leu	Leu	Ser
130						135					140				
Asp	Lys	Asn	Phe	Lys	Phe	Ser	Pro	Leu	Tyr	Arg	Leu	Leu	His	Glu	Arg
145					150				155						160
Leu	Ser	Asn	Ala	Ala	Val	Lys	Lys	Cys	Asp	Tyr	Met	Ile	Ile	Thr	Thr
			165						170					175	
Asp	Phe	Leu	Val	Gly	Cys	Gly	Tyr	Thr	Pro	Ser	His	Cys	Pro	Arg	Thr
		180						185					190		
Leu	Arg	Asn	Met	Glu	Gln	Leu	Leu	Val	Glu	Gln	Cys	Gly	Phe	Ser	Ser
195						200						205			
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210						215					220				
Tyr	Ile	Ala	Asn	Pro	Ile	Thr	Gly	Ser	Tyr	Ser	Asn	Met	Cys	Leu	Ile
225					230					235				240	
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	290					295					300				
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305					310					315				320	
Ser	Leu	Arg	Asp	Val	His	Lys	Lys	Ser	Ser	Ile	Ala	Thr	Ser	Arg	Tyr
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 355 360 365
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 370 375 380
 Gly Glu Arg Arg Pro Arg Leu Ile Met Ser Ile Thr Gly Ser Asp Ala
 385 390 395 400
 Pro Ile Cys Ile Arg Asp Ser Val Arg Asn His Phe Lys Thr Arg Leu
 405 410 415
 Phe Ser Arg Thr Ser Gly Asn Ser Ile Thr Phe Ala Val Pro Pro Gly
 420 425 430
 Glu Arg Glu Leu Met Glu Met Val Arg Glu Val Thr Gly Thr Asp Ile
 435 440 445
 Lys Ile Phe Met Asp Asn Gly Lys Val Tyr Gln Asn Gly Ala Glu Ile
 450 455 460
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 465 470 475 480
 Glu Glu Asn Leu Pro Glu Asp Glu Arg Lys Arg Leu Arg Arg Glu Arg
 485 490 495
 Arg Met Ile Phe Asn Thr Ser Arg Ala Ile Ser Met Tyr Asn Glu Glu
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 Arg Gly Asp Gly Gly Ser Gly Gly Glu Thr Ser Glu Asp Gly Asp Gly
 515 520 525
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 <213> SHRIMP

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<400> 25

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Glu	Val	Tyr	Arg	Met	His	Arg	Arg	Ala	Val	Pro	Thr	Leu	Glu	Glu	Lys	35	40	45	
Asn	Arg	Thr	Ala	Leu	Arg	Tyr	Ser	Asp	Trp	Ser	Pro	Val	Tyr	Arg		50	55	60	
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Arg	Val	Asp	Val	Arg	Asn	Pro	Ser	Arg	Thr	Ala	Ala	Ile	Phe	Val	Pro	100	105	110	
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Ser	Ala	Thr	Glu	Pro	Asn	Ile	Ser	Ile	Gly	Pro	Met	Ser	His	Val	Lys	195	200	205	
Ile	Lys	Leu	Gly	Tyr	Tyr	Asp	Glu	Glu	Asn	Ala	Thr	Ala	Val	Gly	Val	210	215	220	
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Pro	Arg	Gly	Glu	Asp	Ala	Met	Glu	Glu	Asp	Asp	Gly	Glu	Glu	Ala	Asp	275	280	285	
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Gln	Ala	Met	Ser	Ser	Ala	Tyr	Ser	Ser	Val	Ser	Ile	Asp	Ile	Asn	Ser	305	310	315	320
Ser	Ser	Phe	His	Lys	Cys	Phe	Leu	Ile	Lys	Pro	Lys	Tyr	Asn	Ser	Ile	325	330	335	
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Asn	Thr	Arg	Gly	Arg	Glu	Val	Glu	Phe	His	Asp	Arg	Leu	Pro	Ser	Gly	355	360	365	
Ala	Gln	Asp	Asn	Ser	Tyr	Ser	Ile	Val	Lys	Tyr	Met	Lys	Ile	Val	Ser	370	375	380	
Leu	Lys	Glu	Gly	Leu	Lys	Val	Val	Asn	Pro	Ile	Ile	Asn	Thr	Glu	Leu	385	390	395	400
Tyr	Lys	Lys	Lys	Gln	Ala	Leu	Lys	Val	His	Val	Leu	Asn	Met	Thr	Arg	405	410	415	
Asp	Val	Val	Gly	Leu	Asp	Thr	Ser	Glu	His	Ser	Phe	Gly	Val	Ile	Val	420	425	430	
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<210> 26

<211> 2352

<212> DNA

<213> SHRIMP

<400> 26

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<210> 27

<211> 781

<212> PRT

<213> SHRIMP

<400> 27

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 35          40          45
Ile Glu Thr Ile Gly His Phe Leu Ile His Asn His Asn Gln Gly Glu
 50          55          60
Ser Tyr Gln Ile Ala Ser Ser Val Leu Glu Lys Phe Pro Ala Leu Leu
 65          70          75          80
Asn Cys Ile Trp Asn Gly Glu Ser Gly Gly Met Ala Leu Trp Lys Ala

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PCT/US00/28888

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Lys	Ile	Lys	Asn	Trp	Pro	Ser	Val	Ala	Val	Ile	Pro	Ile	Tyr	Gly	Ser
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Val	Cys	Asp	Arg	Glu	Glu	Arg	Pro	Ile	Ile	Met	Ser	Glu	Ile	Ile	Asp
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Lys	Glu	Thr	Leu	Gln	Thr	Ile	Cys	Lys	Ser	Asp	Ile	Arg	Ser	Leu	Leu
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Gly	Met	Met	Asn	Ala	Lys	His	Gly	Thr	Leu	Gly	Gly	Asn	Phe	Leu	His
				165					170					175	
Phe	Tyr	Ala	Arg	Ser	Thr	Lys	Pro	Phe	Glu	Asn	Phe	Gln	Tyr	Glu	Ala
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Ala	Asp	Val	Tyr	Gly	Asn	Asn	Pro	Val	Glu	Ile	Ala	Ile	Ser	Gly	Asp
225					230					235					240
Asp	Asp	Asn	Met	Leu	Leu	Asn	Leu	Ile	Cys	Asn	Tyr	Gly	Val	Ser	Tyr
				245					250					255	
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Gly	Ser	Glu	Gln	Glu	Ser	Tyr	Lys	Leu	Ser	Cys	Gly	His	Phe	Leu	His
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Val	Lys	Cys	Leu	Arg	Asn	Ile	Cys	Ile	Val	Ser	Gln	His	Leu	Arg	Cys
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Glu	Lys	Cys	Leu	Lys	Arg	Phe	Asp	Glu	Ser	Ile	Leu	Arg	Lys	Cys	Thr
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			370			375					380				
Glu	Glu	Ile	Cys	Phe	Met	Arg	Asn	Lys	Lys	Leu	Val	Asp	Asp	Phe	Arg
385					390					395					400
Lys	Leu	Leu	Ser	Pro	Val	Ser	Ile	Pro	His	Phe	Phe	Lys	Asn	Ser	Arg
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Gln	Arg	Asn	Leu	Asp	Met	Leu	Cys	Pro	Tyr	Ser	Asp	His	Thr	Ile	Ile
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 Ala Ile Asn Glu Asn Asn Lys Glu Glu Glu Asp Ala Arg Ile Lys Arg
 595 600 605
 Ala Val Asp Met Ala Val Ala Ala Thr Asn Glu Lys Asn Lys Lys Glu
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 Glu Asp Ala Arg Ile Lys Arg Ile Ile Asp Leu Thr Val Asp Met Arg
 625 630 635 640
 Ile Gln Arg Ile Val Asp Met Ala Ile Ala Ala Ala Thr Lys Lys Asp
 645 650 655
 Lys Lys Glu Glu Glu Lys Arg Thr Lys Arg Glu Gln Glu Leu Arg Ala
 660 665 670
 Asp Leu Arg Arg Ala Met Asp Met Val Asn Glu Val Gln Lys Lys Leu
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 Glu Asp Met Glu Leu Glu Lys Gly Cys Asn Lys Asp Glu Ala Lys Asn
 690 695 700
 Thr Ser Asn Val Val Ser Ser Ser Ser Val Val Ala Tyr Ser Lys Glu
 705 710 715 720
 Ile Val Pro Cys Leu Gly Asn Asn Asn Asn Ala Val Ile Gly Met Thr
 725 730 735
 Ser Thr Asn Tyr Ser Ala Asn Asn Thr Lys Asn Asn Val Phe Gly Ser
 740 745 750
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<211> 1506

<212> DNA

<213> SHRIMP

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 gagggagata tatcctcaag tcccctatat actcagataa tgaagcatat ttcaccagag 420
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 <212> PRT
 <213> SHRIMP

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			20					25					30		
Phe	Ser	Leu	Ser	Gly	Asp	Lys	Tyr	Asp	Thr	Tyr	Glu	Asp	Ile	Leu	Leu
		35					40					45			
Glu	Gln	Phe	Asn	Cys	Phe	Lys	Thr	Ser	Ser	Pro	Ser	Ser	Ala	Arg	Lys
	50					55					60				
Ser	Glu	Ile	Glu	Asp	Lys	Thr	Leu	Ile	Phe	Gln	Leu	Lys	Glu	Gly	Glu
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Lys	Phe	His	Leu	Ala	Lys	Gly	Ile	Glu	Glu	Leu	Arg	Glu	Ile	Leu	Asp
				85					90					95	
Asp	Asn	Ser	Ala	Thr	Ile	Glu	Pro	Ile	Ile	Ser	Pro	Thr	Thr	Phe	Asn
			100					105					110		
Asp	Arg	Asn	Glu	Leu	Leu	Asn	His	Glu	Gly	Asp	Ile	Ser	Ser	Ser	Pro
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Leu	Tyr	Thr	Gln	Ile	Met	Lys	His	Pro	Glu	His	Asp	Ile	Tyr	Glu	Leu
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Asp	Leu	Ile	Val	Gly	Thr	Asp	Leu	Leu	Phe	Gly	Leu	Gly	Val	Asn	Leu
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Arg	Asn	Val	Ser	Lys	Leu	Met	Lys	Lys	Ile	Ser	Tyr	Gly	Thr	Leu	Asn
				165					170					175	
Val	Val	Asp	Val	Cys	His	Arg	Lys	Phe	Phe	Asn	Asn	Arg	Ile	Ile	Val
			180					185					190		
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		210				215					220				
Phe	Asn	Gly	Ile	Cys	Asp	Asp	Val	Glu	Arg	Tyr	Ile	Asn	Ser	Tyr	Phe
225					230					235					240
Phe	Tyr	Pro	Glu	Asn	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Ala	Pro	Ser	Ser
				245						250				255	
Pro	Glu	Met	Glu	Ile	Ala	Asp	Glu	Glu	Glu	Gln	Ser	Pro	Lys	Thr	Ile
			260					265					270		
Lys	Arg	Asn	Asp	Asn	Ala	Ser	Arg	Asn	Trp	Ser	Gly	Val	Cys	Leu	Ile
		275					280					285			
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305					310					315					320
Glu	Lys	Arg	Cys	Lys	Ile	Thr	Asp	Ile	Asn	Gly	Asn	Lys	Pro	Arg	Leu
				325					330					335	
Val	Met	Val	Ile	Thr	Gly	Cys	Tyr	Thr	Glu	Leu	Tyr	Phe	Lys	Asp	Ala
			340					345					350		
Leu	Lys	Gln	Ile	Gly	Glu	Asn	Arg	Arg	Lys	Phe	Leu	Lys	Met	Asn	Gly
		355				360						365			
Asn	Tyr	Phe	Ser	Leu	Ile	Asp	Glu	Gln	Ala	Asp	Leu	Ile	Glu	Phe	Ala
	370					375					380				
Met	Ser	Val	Ser	Gly	Ala	Gly	Glu	Arg	Ile	Phe	Val	Asn	Gly	Leu	Gly
385					390					395					400
Met	Phe	Gln	Asn	Arg	Lys	Met	Ile	Pro	Val	Ile	Asp	Pro	Leu	Thr	Tyr
				405					410					415	
Glu	Asn	Val	Val	Cys	Gly	Glu	His	Asp	Ile	Gln	Lys	Glu	Asp	Ala	Ile
			420					425					430		
Leu	Ser	Val	Arg	Arg	Ala	Ile	Ala	Asp	Tyr	Asn	Asp	Phe	Val	Ser	Lys

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      435      440      445
Asn Lys Arg Gly Lys Lys Arg Ser Ala Glu Glu Glu Asn Glu Asp Glu
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Asp Ala Asp Ala Ser Ser Ser Ser Ser Ser Pro Pro Pro Ser Ser
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Pro Pro Ala His Lys Lys Ser Arg Leu Pro Asp Glu Gly Glu Lys Cys
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Thr Leu Cys

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 <211> 846
 <212> DNA
 <213> SHRIMP

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gtaagcgagg aagatatattga aggtttcgtc gcttctactt ttaaggaggt atcagattca 420
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gacagtggca atactaaaaa attgttgtat gggttaagga ataaaaaagc aggtttatagc 660
tgtttgtgta gaatttttgc agaaattgaa tcagatggga ttatggccaa tacaaatatc 720
ggtgtcgcgtg aaaacaacag agatgaaatt gatgaaaacg aagaaggtaa atatggtttt 780
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<210> 31
 <211> 282
 <212> PRT
 <213> SHRIMP

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 <223> Xaa = Any Amino Acid

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      20      25      30
Thr Val Phe Asp Thr Lys Asn Gln Ala Gly Phe Asp Met Arg Arg Gln
      35      40      45
Val Glu Ala Ala Leu Tyr Glu Ala Ile Ser Lys Lys Lys Glu Lys Ala
      50      55      60
Ile Lys Ala Phe Asp Glu Leu Ile Gln Glu Arg Gly Asp Glu Ile Thr
      65      70      75      80
Pro Leu Thr Thr Met Gln Tyr Glu Glu Trp Val Asn Arg Thr Ile Thr
      85      90      95
Pro Ser Leu Thr Thr Glu Asn Leu Leu Gly Asp Val Glu His Ala Asp
      100      105      110
Phe Leu Leu Asp Arg Met Thr Pro Val Ser Glu Glu Asp Ile Glu Gly
      115      120      125
Phe Ala Ala Ser Thr Phe Lys Glu Val Ser Asp Ser Lys Thr Ala Thr

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130		135		140
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145		150		155
Asn Leu Ala Pro Ser Phe Gly Val Thr Gln Glu Ile Lys Ile Tyr Arg				160
	165		170	175
Ser Asn Asn Ser Ser Glu Leu Asp Asn Val Ala Asp Ser Phe His Ile				
	180		185	190
Tyr Lys Ile Ser Ala Thr Asp Ser Asp Ser Gly Asn Thr Lys Lys Leu				
	195		200	205
Leu Tyr Gly Leu Arg Asn Lys Lys Ala Gly Tyr Thr Cys Leu Cys Arg				
	210		215	220
Ile Phe Ala Glu Ile Glu Ser Asp Gly Ile Met Ala Asn Thr Asn Ile				
225		230		235
Gly Val Ala Glu Asn Asn Arg Asp Glu Ile Asp Glu Asn Glu Glu Gly				
	245		250	255
Lys Tyr Gly Phe Leu Ile Pro Lys Gln Pro Ala Gly Ala Lys Leu Ile				
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 <211> 1089
 <212> DNA
 <213> SHRIMP

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 cttaacgctg tcaaggaaaa acctgcagag tactttgagt tgctaataatc tgcagacact 180
 gaagcagcat taaaaactgc cgaagaaaca gcccttcgag attttgttat tgagaacgac 240
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 ttggcaggcg caacaagcga aacgctaaca aacacaatca tcgcagaggt acaaaaaaag 360
 gcagcattaa taacagaaga agatatcact attaaaatgt taaaacaatt cagggtcgcg 420
 aacaaagata ataaagacgg ggaagcaact cctgaagaaa aggaagattt taccaataat 480
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 aacaaaatat tccctcatga gatgggtttt gaaagatgtg ctattttaat tgaagatttt 600
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 tcagaaagga acttgaggaa tttaccgat tcaaaaccta gacctctaag tgatgcagac 1020
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<210> 33
 <211> 356
 <212> PRT
 <213> SHRIMP

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 Glu Asp Phe Val Lys Gly Arg Leu Leu Asn Ala Val Lys Glu Lys Pro
 35 40 45
 Ala Glu Tyr Phe Glu Leu Leu Ile Ser Ala Asp Thr Glu Ala Ala Leu
 50 55 60

Lys Thr Ala Glu Glu Thr Ala Leu Arg Asp Phe Val Ile Glu Asn Asp
 65 70 75 80
 Ser Val Glu Ile Asp Val Glu Glu Val Leu Glu Glu Lys Pro Arg Glu
 85 90 95
 Tyr Val Phe Lys Leu Ala Gly Ala Thr Ser Glu Thr Leu Thr Asn Thr
 100 105 110
 Ile Ile Ala Glu Val Gln Lys Lys Ala Ala Leu Ile Thr Glu Glu Asp
 115 120 125
 Ile Thr Ile Lys Met Leu Lys Gln Phe Arg Ala Ala Asn Lys Asp Asn
 130 135 140
 Lys Asp Gly Glu Ala Thr Pro Glu Glu Lys Glu Asp Phe Thr Asn Asn
 145 150 155 160
 Ser Asp Leu Val Gly Leu Asn Glu Val Val Glu Lys Thr Thr Asn Ile
 165 170 175
 Val Ile Asn Lys Ile Phe Phe Met Val Phe Glu Arg Cys Ala Ile Leu
 180 185 190
 Ile Glu Asp Phe Asp Thr Gly Val Val Thr Asp Gln Ala Ile Gln Ile
 195 200 205
 Pro Ser Asn Lys Tyr Lys Ile Arg Leu Val Glu Gly Asp Glu Pro Glu
 210 215 220
 Val Phe Pro Gly Asp Cys Leu Asp Leu Ala Val Ser Val Asp Lys Ile
 225 230 235 240
 Asn His Val Leu Lys Ile Ser Ala Lys Asn Gly Cys Glu Asn Asn Cys
 245 250 255
 Phe Val Ile Ile Pro Arg Phe Ser Pro Val Gly Ser Val Ser Ser Met
 260 265 270
 Ile Leu Gly Ser Thr Asp Gln Val Lys Pro Lys Thr Phe Leu Phe Leu
 275 280 285
 Ala Asn Lys Asn Asp Ser Thr His Phe Gln Phe Thr Met Asp Lys Gln
 290 295 300
 His Ser Val Gly Cys Glu Leu Asp Met Leu Ile Phe Ser Asn Leu Arg
 305 310 315 320
 Asn Leu Pro Asp Ser Lys Pro Arg Pro Leu Ser Asp Ala Asp Ile Leu
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 Leu Val Asp Asp
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 <211> 930
 <212> DNA
 <213> SHRIMP

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WO 01/38351

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PCT/US00/28888

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Phe	Cys	Pro	Asp	Val	Leu	Met	Val	His	Arg	Gly	Asp	Ser	Phe	Asn	Ile
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Asn	Phe	Ala	Asn	Asn	Lys	Leu	Glu	Cys	Tyr	Asn	Glu	Arg	Asn	Gly	Ile
705					710					715					720
Glu	Glu	Val	Thr	Ser	Ser	Gln	Thr	Val	Asn	Ala	Lys	Glu	Ala	Leu	Glu
				725						730				735	
Asp	Ile	Thr	Lys	Ile	Lys	Met	Lys	Arg	Gly	Asp	Asp	Ile	Ile	Asp	Val
			740					745					750		
Val	Lys	Ser	Lys	Gly	Leu	Ser	Leu	Arg	Glu	Phe	Ser	Lys	Lys	Val	Ser
		755					760					765			
Lys	Ile	Val	Arg	Arg	Phe	Asn	Glu	Ile	Thr	Asn	Gln	Leu	Cys	Asn	Asn
		770				775					780				
Cys	Asn	Val	Asn	Ser	Ser	Asn	Gly	Asp	Val	Asp	Phe	His	Val	Phe	Thr
785					790					795					800
Ser	Val	Cys	Val	Tyr	Ile	His	Asn	Ile	Ile	Pro	Val	Leu	Glu	Asp	Ile
				805					810					815	
Ser	Ile	Phe	Ala	Glu	Leu	Gly	Glu	Glu	Leu	Thr	Lys	Leu	Val	Lys	Glu
			820					825					830		
Cys	Arg	Asp	Val	Ala	Gly	Glu	Asp	Lys	Thr	Tyr	Asp	Asp	Ile	Ile	Arg
		835					840					845			
Asn	Tyr	Glu	Ile	Thr	Val	Lys	Tyr	Phe	Lys	Leu	Phe	Asn	Ala	Leu	Val

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850						855						860					
Lys	Phe	Cys	His	Arg	Asn	Tyr	Asn	Val	Ala	Val	Thr	Ser	Ala	Ile	Asn		
865					870					875					880		
Arg	Arg	Gly	Tyr	Met	Cys	Met	Val	Ser	Asn	Leu	Val	Gly	Tyr	Tyr	Cys		
				885					890						895		
Lys	Leu	Ser	Asp	Asn	Ala	Ile	Gln	Tyr	His	Glu	Ser	Leu	Cys	Ser	Leu		
			900					905					910				
His	Ser	Ser	Ile	Ser	Tyr	Ala	Asp	Tyr	Tyr	Thr	Ser	Arg	Asn	Asn	Asn		
		915					920					925					
Ser	Glu	Asp	Gly	Gly	Gly	Asn	Ser	Ser	Ser	Glu	Lys	Ser	Asn	Ala	Asp		
	930					935					940						
Val	Ala	Lys	Thr	Met	Ala	Ser	Phe	Tyr	Asp	Gln	Phe	Asp	Lys	Ser	Glu		
945					950					955					960		
Asp	Ser	Lys	Lys	Asn	Lys	Asn	Lys	Thr	Ser	Asn	Glu	Ile	Leu	Ile	Lys		
				965				970						975			
Met	Phe	Gln	Met	Asp	Arg	Val	Leu	Asp	Gly	Met	Asp	Asp	Asp	Asp	Asp		
			980					985					990				
Glu	Asp	Ser	Asp	Ser	Ser	Ser	Ser	Glu	Asn	Glu	Glu	Glu	Glu	Glu	Glu		
		995					1000						1005				
Glu	Glu	Ile	Val	Lys	Lys	Pro	Ala	Lys	Lys	Arg	Lys	Val	Glu	Asp	Val		
	1010				1015					1020							
Asp	Ser	Asn	Lys	Lys	Thr	Leu	Pro	Lys	Glu	Pro	Ala	Val	Lys	Lys	Val		
1025					1030				1035						1040		
Lys	Gln	Glu	Glu	Asp	Val	Glu	Met	Glu	Glu	Val	Lys	Glu	Ala	Ala	Ala		
				1045				1050						1055			
Glu	Glu	Glu	Lys	Lys	Glu	Glu	Gln	Glu	Ala	Lys	Glu	Glu	Asp	Ala	Thr		
			1060				1065						1070				
Glu	Tyr	Asp	Asp	Asp	Thr	Glu	Glu	Asp	Glu	Lys	Ala	Val	Ala	Ser	Asp		
	1075					1080						1085					
Glu	Asp	Glu	Asp	Asp	Glu	Asp	Ser	Lys	Ala	Ile	Phe						
	1090					1095						1100					

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 <211> 618
 <212> DNA
 <213> SHRIMP

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 tttaacatgc agaagtgtc agactgtgct cctttccctc cctaccccg cactgagaag 180
 cctttccctc cataccctgg tactgcagta gaagaggagg agaagcaaaa ggaaattgag 240
 gagcttctgg ttgaccaatc tttccctccc ccattccctg gaaataagct gagagatc 300
 cccagaacct accctctcga atttcccgag aagaaggaga aggatttccc ttgcgttgac 360
 actaccggtc acagcgatat ccccttcacg gatctggaga aaaccccacc ccgtagtgac 420
 gttaggcacg gttaccacta cttaatcaac cccaacaagg ttggggagct taaccatc 480
 gttgtaagc tcaactgaaa gcaagaaaac ctgaacaaat tggtgttgga tgttgatgac 540
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 aagttctcaa aaaactag 618

<210> 45
 <211> 205
 <212> PRT
 <213> SHRIMP

<400> 45
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 Ile Asp Pro Asn Lys Glu Ile Pro Tyr Asn Val Pro Pro Thr Pro Ile
 20 25 30


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      35                      40                      45
Cys Ala Pro Phe Pro Pro Tyr Pro Gly Thr Glu Lys Pro Phe Pro Pro
      50                      55                      60
Tyr Pro Gly Thr Ala Val Glu Glu Glu Glu Lys Gln Lys Glu Ile Glu
      65                      70                      75                      80
Glu Leu Leu Val Asp Gln Ser Phe Pro Pro Phe Pro Gly Asn Lys
      85                      90                      95
Leu Arg Asp Ile Pro Arg Thr Tyr Pro Leu Glu Phe Pro Glu Lys Lys
      100                      105                      110
Glu Lys Asp Phe Pro Cys Val Asp Thr Thr Gly His Ser Asp Ile Pro
      115                      120                      125
Phe Ile Asp Leu Glu Lys Thr Pro Pro Arg Ser Asp Val Arg His Gly
      130                      135                      140
Tyr His Tyr Leu Ile Asn Pro Asn Lys Val Gly Glu Leu Asn His Ile
      145                      150                      155                      160
Val Gly Lys Leu Thr Glu Lys Gln Glu Asn Leu Asn Lys Leu Val Leu
      165                      170                      175
Asp Val Asp Asp Val Val Ile Asn Leu Ser Ser Thr Leu Lys Glu Leu
      180                      185                      190
Glu Lys Leu Arg Ala Gly Leu Cys Lys Phe Ser Lys Asn
      195                      200                      205

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<210> 46
 <211> 630
 <212> DNA
 <213> SHRIMP

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gttagcgccg cctgggtgcc tgttgatgaa gaggatgaag atagggagga aatgagaaga 180
cttgaagatt tttcttcaga tgaagaagac gatgataata aatcatgtca ttgtgaccat 240
agcgatgacg atgacgatga cgaggaggat ccttcatgct ttaagggttt ttcagctggc 300
ctgtgctctt ttgtgagggg tttctttggc ttccctcagga agtcacttac caagaaacag 360
gtgttccttc ttacaagcgc agccgttgct gctattttta agactagaga tgtggctaaa 420
actgaagaag gcgcagcaac catggaagaa aattcaacag atgtgattac tggaggagat 480
ggagatagtg gtattgctgc tgatgttgtc tctctcgcta gtgagggaga gggagaaaat 540
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<210> 47
 <211> 207
 <212> PRT
 <213> SHRIMP

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      20      25      30
Val Asn Lys Pro Thr Pro Val Ser Ala Ala Trp Val Pro Val Asp Glu
      35      40      45
Glu Asp Glu Asp Arg Glu Glu Met Arg Arg Leu Glu Asp Phe Ser Ser
      50      55      60
Asp Glu Glu Asp Asp Asp Asn Lys Ser Cys His Cys Asp His Ser Asp
      65      70      75      80
Asp Asp Asp Asp Asp Glu Glu Asp Pro Ser Cys Phe Lys Gly Phe Ser
      85      90      95
Ala Gly Leu Cys Ser Phe Val Arg Gly Phe Phe Gly Phe Leu Arg Lys

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	100		105		110										
Ser	Leu	Thr	Lys	Lys	Gln	Val	Phe	Leu	Leu	Thr	Ser	Ala	Ala	Val	Ala
	115						120					125			
Ala	Ile	Phe	Lys	Thr	Arg	Asp	Val	Ala	Lys	Thr	Glu	Glu	Gly	Ala	Ala
	130						135					140			
Thr	Met	Glu	Glu	Asn	Ser	Thr	Asp	Val	Ile	Thr	Gly	Gly	Asp	Gly	Asp
	145					150					155				160
Ser	Gly	Ile	Ala	Ala	Asp	Val	Val	Ser	Leu	Ala	Ser	Glu	Gly	Glu	Gly
			165						170					175	
Glu	Asn	Gly	Ser	Leu	Leu	Glu	Ser	Ile	Ala	Thr	Thr	Leu	Ile	Lys	Thr
			180					185					190		
Thr	Ile	Glu	Asn	Leu	Val	Asp	Gly	Gly	Glu	Glu	Thr	Thr	Glu	Leu	
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<210> 48
 <211> 2685
 <212> DNA
 <213> SHRIMP

<400> 48

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gacaatatca cagacaaaaa cattcagtta ttgaacaaga aattgggtaa gaaaacagca 180
aagaaaataa agaaggaaga tgcacctgaa acaaaggaaa atagtgcga agacatatat 240
gccaccaagg aattcgaaca gacaataaaa ggtctacaga caaaaaaagg tgccaccgag 300
gaaaacgccca tcgcggccgc agctgccgct gccactgctg ctgcggtaga aaaggctatg 360
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cccggtatgt ttttcaagct gcgagtgcgc gcaaagcctc tcttgccctg agagactata 780
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aatttgaata aactattagt ttctgctatc aaggaaacag gagccactga aactgaagca 2580
cagatattca acaagattat tggtagttaa aagggaactat caattctctg tcaacttgtg 2640
gaaaggagga acaaagacaa taatgtcttc gactgatttg tctaa 2685

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<210> 49
 <211> 886
 <212> PRT
 <213> SHRIMP

<400> 49

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			20					25					30		
Val	Ser	Leu	Asp	Ile	Asp	Phe	Lys	Asp	Asn	Ile	Thr	Asp	Gln	Asn	Ile
		35					40					45			
Gln	Leu	Leu	Asn	Lys	Lys	Leu	Gly	Lys	Lys	Thr	Ala	Lys	Lys	Ile	Lys
		50					55				60				
Lys	Glu	Asp	Ala	Pro	Glu	Thr	Lys	Glu	Asn	Ser	Asp	Glu	Asp	Ile	Tyr
65					70				75					80	
Ala	Thr	Lys	Glu	Phe	Glu	Gln	Thr	Ile	Lys	Gly	Leu	Gln	Thr	Lys	Lys
				85					90					95	
Gly	Ala	Thr	Glu	Asn	Ala	Ile	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Thr
			100				105						110		
Ala	Ala	Ala	Val	Glu	Lys	Ala	Met	Leu	Ser	Glu	Ser	Glu	Gly	Lys	Ser
		115					120					125			
Met	Val	Ile	Asn	Arg	Ala	Arg	Met	Val	Leu	Ser	Lys	Arg	Asp	Thr	Ser
	130					135					140				
Gln	Lys	Gln	Phe	Thr	Ala	Leu	Lys	Asn	Arg	Glu	Ser	Phe	Phe	Ser	Val
					150					155					160
Leu	Ile	Phe	Glu	Thr	Gly	Ser	Val	Ile	Val	Val	Gly	Leu	Gln	Asp	Pro
				165					170					175	
Ser	Leu	Thr	Lys	Leu	Cys	Val	Ile	Lys	Ala	Thr	Thr	Asp	Ile	Ala	Asp
			180					185					190		
Ile	Leu	Gln	Lys	Asn	Ile	Ser	Val	Ala	Asn	Val	Ser	Ile	Val	Asn	Thr
		195					200					205			
Val	Ser	Thr	Phe	Asn	Arg	Phe	His	Leu	Asn	Phe	Ile	Arg	Leu	Gly	Lys
		210				215					220				
Phe	Phe	Glu	Arg	Asn	Cys	Ile	Ser	Tyr	Ser	Tyr	Asn	Pro	Glu	Thr	Phe
225					230					235					240
Pro	Gly	Met	Phe	Phe	Lys	Leu	Arg	Val	Pro	Ala	Lys	Pro	Leu	Leu	Pro
				245					250					255	
Gly	Glu	Thr	Ile	Gly	Glu	Tyr	Tyr	Thr	Lys	Val	Ala	Met	Met	Arg	Asp
			260					265					270		
Ser	Lys	Asp	Pro	Asn	Phe	Lys	Met	Ser	Asp	Trp	Leu	Arg	Ile	Lys	Thr
		275					280					285			
Ala	Leu	Thr	Phe	Lys	Val	Gly	Lys	Ile	Thr	Val	Leu	Gly	Glu	Gly	Glu
		290				295					300				
Ser	Gly	Cys	Gly	Asp	Val	Ser	Val	Val	Ser	Lys	Leu	Leu	Phe	Gly	Leu
305					310					315					320
Phe	His	Tyr	Phe	Met	Asp	Asn	Asn	Ile	Lys	Met	Ser	Pro	Lys	Glu	Ala
				325					330					335	
Gln	Arg	Val	Arg	Glu	Lys	Tyr	Gly	Ile	Pro	His	Leu	Glu	Trp	Tyr	Leu
				340				345					350		
Tyr	Ile	Asp	Met	Leu	Leu	His	Ser	Tyr	Pro	Tyr	Val	Lys	Pro	Ser	Ala
		355					360					365			
Glu	Gln	Val	Lys	Arg	Ala	Met	Val	Asp	Gln	Gln	His	Glu	Val	Asp	Arg
		370				375					380				
Thr	Tyr	Tyr	Gly	Thr	Lys	Asn	Ser	Met	Asp	Ala	Ala	Met	Ser	Ala	Asn

385					390					395					400
Leu	Val	Pro	Ser	Lys	Glu	Glu	Ser	Ile	Ser	Phe	Ile	Lys	Lys	Ile	Arg
				405					410					415	
Ser	Gln	Gln	Leu	Phe	Gly	His	Leu	Cys	Lys	Pro	Ser	Lys	Glu	Thr	Thr
			420					425					430		
Arg	Arg	Ala	Ile	Asp	Thr	Leu	Ser	Phe	Asp	Pro	Ile	Asn	Gln	Asp	Arg
		435					440					445			
Trp	Trp	Asn	Lys	Asn	Asp	Gln	Tyr	Tyr	Gly	Lys	Glu	Arg	Cys	Asp	Pro
	450					455					460				
Phe	Ser	Val	Ala	Arg	Leu	Val	Ser	Val	Ser	Glu	Asn	Thr	Asn	Ser	Met
465					470					475					480
Met	Asn	Ser	Arg	Ile	Ser	Cys	Gln	Gly	Lys	Trp	Trp	Leu	Asp	Glu	Asn
				485					490					495	
Glu	Tyr	Lys	Asp	Lys	Leu	Asp	His	Ile	Val	Asp	Leu	Cys	Thr	Glu	Glu
			500					505					510		
Ile	Val	Glu	Glu	Cys	Glu	Ser	Lys	Gly	Phe	Ile	Asp	Phe	Leu	Arg	Lys
		515					520					525			
His	Gln	Lys	Glu	Lys	Ile	Pro	Thr	Pro	Tyr	Val	Leu	Leu	Ala	Arg	Ala
	530					535				540					
Cys	Asn	Gln	Lys	Asn	Gly	Asn	Lys	Met	Ser	Ile	Asn	Asn	Asn	Ser	Asn
545					550					555					560
Tyr	Leu	Ser	Gly	Ser	Ser	Arg	Ala	Lys	Arg	Asn	Ala	Lys	Leu	Gln	Glu
			565						570					575	
Lys	His	Arg	Val	Thr	Leu	Ala	Arg	Leu	Asn	Thr	Met	Met	Ala	Ser	Tyr
			580					585					590		
Arg	Phe	Leu	Asn	Asn	Tyr	Ile	Ser	Thr	Asp	Ile	Ala	Pro	Asp	Phe	Ala
		595					600					605			
Lys	Leu	Phe	Gly	Asn	Asp	Val	Tyr	Ser	Leu	Leu	His	Leu	Met	Thr	Asn
	610					615					620				
Leu	Lys	Ser	Arg	Gly	His	Ala	Leu	Thr	Tyr	Asn	Glu	Arg	Ala	Leu	Ser
625					630					635					640
Ser	Asn	Glu	Ser	Thr	Tyr	Lys	Thr	Pro	Gly	Asn	Ala	Tyr	Phe	Ser	Thr
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Leu	Phe	Glu	Lys	Ser	Ile	Ile	Asn	Asn	Gln	Glu	Thr	Ala	Asn	Lys	Gly
			660					665					670		
Asn	Asn	Arg	Lys	Arg	Lys	Phe	Ser	Arg	Ile	Gly	Gln	Glu	Lys	Ser	Ser
		675				680						685			
Phe	Leu	Cys	Asn	Ala	Cys	Gly	Val	Asn	Leu	Asn	Lys	Gly	Ser	Asp	Glu
	690					695					700				
Ile	Ile	Lys	Gly	Ile	Cys	Thr	Ser	Cys	Asp	Gln	Asn	Ser	Thr	Ser	Tyr
705					710					715					720
Ile	Glu	Asn	Ala	Leu	Ser	Asp	Ile	Asn	Arg	Asp	Lys	Lys	Ile	Lys	Arg
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Phe	Lys	Ala	Ala	Ala	Thr	His	Pro	Pro	Val	Lys	Gln	Glu	Leu	Val	Asp
			740					745					750		
Ser	Leu	Ser	Ser	Ser	Ser	Ser	Pro	Ser	Ser	Ser	Ser	Ser	Gln	Thr	Ser
		755					760					765			
Asn	Lys	Asn	Asn	Arg	Cys	Thr	Pro	Ser	Asp	Phe	Ile	Asp	Tyr	Val	Tyr
	770					775					780				
Lys	Phe	Thr	Asp	Glu	Thr	Thr	Gly	Ala	Pro	Lys	Val	Gly	Leu	Val	Phe
785					790					795					800
Lys	Met	Cys	Asp	Ile	Leu	Ala	Ser	Leu	Ala	Ser	Arg	Arg	Gly	Met	Glu
				805					810					815	
Asp	Arg	Pro	Thr	Ala	Asn	Tyr	Arg	Thr	Ser	Leu	His	Ser	Ala	Thr	Gln
			820					825					830		
Asn	Lys	Thr	Asn	Leu	Asn	Lys	Leu	Leu	Val	Ser	Ala	Ile	Lys	Glu	Thr
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Gly	Ala	Thr	Glu	Thr	Glu	Ala	Gln	Ile	Phe	Asn	Lys	Ile	Ile	Gly	Ser
	850					855					860				
Glu	Lys	Gly	Leu	Ser	Ile	Leu	Cys	Gln	Leu	Val	Glu	Arg	Arg	Asn	Lys
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Asp Asn Asn Val Phe Asp
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<210> 50
<211> 1268
<212> DNA
<213> SHRIMP

<400> 50
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<213> SHRIMP

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35 40 45
Val Thr Lys Phe Ser Cys Asn Gln Gln Ser Gly Arg Cys Ala Arg Ser
50 55 60
Val Tyr Ser Ala Ser Ser Leu Glu Arg Ala Ala Asn Asp Leu Gly His
65 70 75 80
Ile Ile Gly Ile Ile Lys Lys Asn Pro Lys Leu Glu Glu Glu Leu Pro
85 90 95
Glu Ser Phe Leu Trp Phe Ile Asn His Asn Gly Gly Asp Leu Phe Val
100 105 110
Asn Lys Arg Ala Ala Tyr Tyr Asp Thr Met His Leu Ser Ile Gly Lys
115 120 125
Leu Asp Asn Val Asp Thr Leu Ala Gln Gly Leu Asp Lys Arg Met Ala
130 135 140
Ser Ser Leu Arg Glu His Leu Leu Arg Lys Leu Asp Ser Ile Leu Leu
145 150 155 160
Gln Ile Asp Lys Val Lys Tyr Glu Lys Ala Lys Lys Trp Ile Leu Asp
165 170 175

Ile Thr Gln Glu Ala Gly Thr Glu Glu Asp Asn Lys Glu Glu Glu Asp
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 Ala Lys Lys Glu Asp Gln Ser Leu Ser Val Ser Glu Ile Val Asp Val
 195 200 205
 Leu Thr Gly Thr His Asp Pro Met Pro Leu Arg Arg Phe Ile Gln Lys
 210 215 220
 Lys Ile Tyr Pro Leu Ser Arg Asn Glu Leu Arg Glu Leu Ala Leu Lys
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 Glu Leu Phe Pro Glu Glu Thr Thr Ser Pro Gln Val Leu Ser Arg Gln
 245 250 255
 His Asp Val Ser Thr Arg Glu Asp Leu Cys Asn Glu Ser Met Asn Ala
 260 265 270
 Gly Arg Ala Glu Ser Ile Phe Ser Asp Pro Asp Ser Gly Glu Tyr Val
 275 280 285
 Ala Thr Cys Ala Cys Lys Glu Tyr Leu Thr Gly Pro Ala Cys Lys His
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 Lys Tyr Tyr Val Ile Asp Tyr Asp Lys Trp Lys Arg Thr Gly Arg Pro
 305 310 315 320
 Glu Phe Leu Thr Asp Pro Val Leu His Phe Lys Lys Ala Glu Ala Val
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 Cys Lys Ser Thr Asn Pro Asn Leu Arg Ala Ile Tyr Ser Pro Asp Asn
 340 345 350
 Lys Gly Phe Leu Cys Ala Pro Val Ala Glu Leu Val Lys Thr Ala Leu
 355 360 365
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<210> 52
 <211> 1401
 <212> DNA
 <213> SHRIMP

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1401

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<211> 459

<212> PRT

<213> SHRIMP

<220>

<221> VARIANT

<222> (1)...(459)

<223> Xaa = Any Amino Acid

<400> 53

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Gln	Ser	Pro	Glu	Glu	Ala	Ala	Ala	Leu	Ser	Val	Tyr	Gly	Ala	Pro	Pro
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Lys	Pro	Ser	Ala	Ser	Ala	Val	Ala	Ser	Ile	Ile	Thr	Gly	Glu	Arg	Thr
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Ser	Leu	Asn	Asp	Lys	Tyr	Leu	Ser	Asp	Asn	Val	Leu	Leu	Lys	Met	Ser
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Val	Ala	Arg	Val	Gly	Gln	Glu	Asn	Asn	Arg	Lys	Arg	Ala	Asp	Gln	Ala
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	115						120					125			
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	130					135					140				
Thr	Met	Asp	Thr	Ser	Ile	Ser	Ser	Glu	Pro	Leu	Ser	Leu	Thr	Asp	Phe
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Phe	Ser	Lys	Val	Asp	Ser	Ala	Arg	Ser	Thr	Arg	Phe	Asp	Ala	Phe	Val
		180						185				190			
Asn	Gly	Val	Ala	Asn	Asn	Met	Asp	Ile	Lys	Ser	Ser	Ile	Asp	Trp	Ala
	195					200						205			
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Cys	Ser	Val	Asp	Thr	Ile	Val	Ser	Arg	Asp	Ala	Ser	Val	Val	Lys	Thr
225				230						235				240	
Ala	Val	Asn	Asp	Ile	Tyr	Ala	Ser	Val	Gly	Lys	Ser	Tyr	Cys	Arg	Pro
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Ala	Thr	Gln	Leu	Thr	Phe	Met	Ser	Glu	Ile	Glu	Lys	Leu	Arg	Lys	Ala
		260						265					270		
Ala	Val	Val	Cys	Phe	Glu	Ala	Leu	Met	Ser	Asp	Thr	Arg	Glu	Arg	Ala
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Phe	Val	Glu	Phe	Leu	Phe	Tyr	Val	Ser	Phe	Lys	Glu	Asp	Asn	Thr	Asn
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Ser	Lys	Leu	Phe	Val	Gln	Asn	Lys	Leu	Ser	Ser	Met	Ser	Gly	Asn	Pro
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Arg	Gln	Pro	Ile	Lys	Leu	Val	Arg	Arg	Ser	Ala	Glu	Glu	Thr	Leu	Phe
			325						330				335		
Gly	Leu	Cys	Phe	Met	Phe	Lys	Val	Met	Pro	Pro	Glu	Phe	Met	Asn	Cys
		340						345				350			
Ile	Phe	Asn	Phe	Pro	Thr	Ile	Pro	His	Ser	Thr	Gln	Tyr	His	Gly	Gly
	355					360					365				
Thr	Cys	Leu	Thr	Pro	Leu	Leu	Arg	Lys	Tyr	Gly	Ser	Ser	Phe	Glu	Lys
	370					375					380				

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Ser Trp Ala His Phe Glu Glu Ile Leu Ser Ala Asn Ala Val Lys Lys
 385 390 395 400
 Phe Gly Val Asn Asp Thr Arg Ile Asp Cys Leu Asp Ala Val Ala Asn
 405 410 415
 Leu Thr Gly Pro Val Tyr Val Leu Ile Leu Asp Leu Val Arg Thr Leu
 420 425 430
 Ser Ala Gln Arg Ser Cys Ser Thr Lys Phe Leu Arg Glu Ile Lys Glu
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 Asn Tyr Leu Leu Trp Asn Arg Phe Val Ser Xaa
 450 455

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 <213> SHRIMP

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 agttcatcca catcttctaa gaagaagagc aaatccaata aacacaccaa gaccaaggaa 180
 gaacaacttc tagaattcgt gaaggatctg gagcggagcg accccactgt tcctgatgag 240
 aagggtcaagc aagaagttga agaaaagtcc cctgaagcta ttgctgaaat tttttcaatg 300
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 <211> 272
 <212> PRT
 <213> SHRIMP

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 20 25 30
 Glu Pro Pro Ser Phe Glu Asp Lys Ser Ser Ser Thr Ser Ser Lys Lys
 35 40 45
 Lys Ser Lys Ser Asn Lys His Thr Lys Thr Lys Glu Glu Gln Leu Leu
 50 55 60
 Glu Phe Val Lys Asp Leu Glu Arg Ser Asp Pro Thr Val Pro Asp Glu
 65 70 75 80
 Lys Val Lys Gln Glu Val Glu Glu Lys Ser Pro Glu Ala Ile Ala Glu
 85 90 95
 Ile Phe Ser Met Phe Gly Ile Ala Gln Asp Ser Lys Phe Lys Ser Leu
 100 105 110
 Leu Pro Ile Glu Arg Ile Lys Ser Ile Thr Thr Lys Ile Val Ile Asp
 115 120 125
 Ala Ile Asn Gln Pro Val Arg Lys Met Leu Val Asp His Leu Tyr His
 130 135 140
 Phe Lys Glu Met Gln Asn Val Val Glu Lys Tyr Lys Asp Asp Ser Asp
 145 150 155 160
 Glu Lys Leu Ser Val Ile Leu Lys Ser Lys Lys Ser Pro Lys Glu Phe
 165 170 175

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Asp Leu Ser Phe Ser Asp Tyr Val Asp Arg Leu Asn Arg Ile Leu Val
 180 185 190
 Gly Val Ile Lys Arg Val Ala Gly Ala Ile Glu Ser Lys Glu Leu Leu
 195 200 205
 Gln Ser Asn Ser Met Ile Met Asn Ser Val Leu Gly Thr Val Val Ser
 210 215 220
 Asn Ile Pro Tyr Asn Met Lys Ile Asn Ile Cys Val Phe Leu Thr Asn
 225 230 235 240
 Phe Ile Cys Thr Phe Ala Asn Asp Asp Leu Tyr Thr Phe Phe Arg Asp
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 Asp Glu Lys Phe Val Met Ser Gln Val Thr Arg Tyr Ile Ser Lys Asp
 260 265 270

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 <211> 1398
 <212> DNA
 <213> SHRIMP

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 gtggtttctt cgactttaca agaagctaata ctcgttacca ctgaaaaaga taaacctgtt 240
 caatttgtaa gaggtttagt cccagaaaaa atgatggaaa aatatagatc ggacttgtct 300
 cctaagaacg tgggggaata tattttacct tcagaaaaag aaacagacaa attgaaaagt 360
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 aacaagagga ttatagggcc aagggatctg attagtagag atgatgtgaa ggacaaaagt 480
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 tgcaccgaca aggtgatgg aatatatcaa gtcaatcaaa agggagggat attatataga 1260
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 <211> 463
 <212> PRT
 <213> SHRIMP

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 35 40 45
 Pro Ser Thr Asn Gly Tyr Ser Gly Cys Thr Thr Asn Val Val Ser Ser
 50 55 60
 Thr Leu Gln Glu Ala Asn Leu Val Thr Thr Glu Lys Asp Lys Pro Val
 65 70 75 80

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Gln Phe Val Arg Gly Leu Val Pro Arg Lys Met Met Glu Lys Tyr Arg
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 Ser Asp Leu Ser Pro Lys Asn Val Gly Glu Tyr Ile Leu Pro Ser Glu
 100 105 110
 Lys Glu Thr Asp Lys Leu Lys Ser Asp Tyr Lys Lys Gly Lys Lys Val
 115 120 125
 Gly Leu Leu Thr Ala Leu Ser Asn Gly His Asp Ser Asn Lys Arg Ile
 130 135 140
 Ile Gly Pro Arg Asp Leu Ile Ser Arg Asp Asp Val Lys Asp Lys Ser
 145 150 155 160
 Tyr Val Phe Lys Arg Leu Ser Lys Asp Pro Leu Val Tyr Tyr Ser Ser
 165 170 175
 Ala Thr Ser Lys Tyr Val Arg Lys Phe Ser Pro Phe Arg Ala Lys Lys
 180 185 190
 Phe Met Thr Ser Thr Gln Leu Gly Ser Lys Leu Val Tyr Pro His Pro
 195 200 205
 Ile Arg Tyr Gly Thr Ala Phe Val Leu Pro Thr Gly Tyr Val Ile Asn
 210 215 220
 Lys Ala Tyr Gly Met Asp Asn Glu Asp Leu His Thr Trp Asn Pro Pro
 225 230 235 240
 Ser Ser Ser Val Leu Val Pro Asp Ser Asn Asn Asp Arg Leu Thr Val
 245 250 255
 Glu Cys Ala Lys Thr Asp Pro Thr Ile Gly Ile Tyr Gly Phe Gly Gly
 260 265 270
 Ser Asp Asp Asn Arg Arg Ala Lys Glu Glu Gly Tyr Val Glu Met Leu
 275 280 285
 Leu Cys Asn Cys Asp Asn His Lys Asp Leu Leu Lys Ala Pro Leu Ile
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 Thr Glu Tyr Ser Thr Asn Pro Thr Glu Ile Gln Val Asp Val Ala Ala
 305 310 315 320
 Lys Arg Val Leu Phe Pro Ala Pro Gly Ser Glu Pro Val Lys Ser Ser
 325 330 335
 Gln Val Thr Ser Ala Ala His Gln Leu Asp Gly Ala Thr Gly Glu His
 340 345 350
 Asp Ile Ser His Glu Pro Val Lys Leu Ser Asp Thr Gly Asp Tyr Ala
 355 360 365
 Val Gly Ser Pro Ile Val Phe Lys Pro Val Tyr Gly Thr Ser Leu Val
 370 375 380
 Asn Leu Pro Glu Thr Gly Ser Pro Leu Ala Leu Asn Cys Pro Cys Thr
 385 390 395 400
 Asp Lys Ala Asp Gly Ile Tyr Gln Val Asn Gln Lys Gly Gly Ile Leu
 405 410 415
 Tyr Arg Asp Met Val Gly Tyr Leu Asn Ala Asn Pro Val Glu Ala Ala
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<210> 58

<211> 2361

<212> DNA

<213> SHRIMP

<400> 58

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<210> 59

<211> 778

<212> PRT

<213> SHRIMP

<400> 59

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35          40          45
Ala Gln Asp Ile Ser Ala Gln Leu Val Thr His Ile Ile Arg Leu Ala
50          55          60
His Cys Ser Glu Ser Asn Lys Ile Lys Asp Thr Ile Ala Ser Ile Ala
65          70          75          80
Gly Leu Phe Ile Asn Asn Ile Phe Asp Asn Asn Ser Thr Lys Asn Lys
85          90          95
Leu Lys Thr Tyr Asn Gln Phe Lys Ala Glu Ser Gln Asn Lys Ser Ser
100         105         110
Val Leu Asn Ile Phe Gly Ser Leu Asp Pro Leu Ser Met Leu Ser Ser
115         120         125
Phe Met Gly Ser Asp Pro Ala Lys Ser Gly Gly Glu Asn Leu Asp Lys
130         135         140
Ser Leu Gly Val Leu Phe Glu Val Leu Gln Asn Tyr Asn Pro Cys Lys

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Gly	Gly	Met	Asn	Leu	Ala	His	Glu	Ile	Thr	Asn	Phe	Ile	Glu	Thr	Ile
				965					970					975	
Ala	Gly	Lys	Glu	His	Thr	Gly	Lys	Glu	Ser	Val	Phe	Leu	Ser	Pro	Arg
			980					985					990		
Leu	Ser	Val	Ile	Leu	Leu	Arg	Tyr	Ile	Trp	Phe	Asn	Ala	Ala	Val	Val
		995					1000					1005			
Ser	Leu	Thr	Asp	Ser	Asn	Ile	Lys	Met	Pro	Leu	Asn	Thr	Met	Ser	Glu
	1010					1015					1020				
Gly	Thr	Gly	Asp	Asp	Ile	Tyr	Arg	Asp	Tyr	Leu	Ala	Ile	Arg	Gly	Met
1025					1030					1035				1040	
Val	Asn	Asn	Tyr	Asn	Ser	Ser	Leu	Ser	Ser	Ile	Ser	Val	Lys	Ala	Ile
				1045					1050					1055	
Ser	Asp	Arg	Tyr	Asn	Cys	Gly	Ser	Gly	Asn	Thr	Ser	Thr	Ser	Asn	Lys
		1060						1065					1070		
Asn	Val	Thr	Ile	Lys	Thr	Gln	Gly	Glu	Leu	Leu	Thr	Val	Leu	Gln	Gln
		1075					1080					1085			
Thr	Ala	Asn	Ala	Leu	Ser	Ala	Phe	Thr	Asn	Lys	Gly	Gly	Val	Gly	Ala
	1090					1095					1100				
Thr	Pro	Asp	Ala	Ala	Asn	Met	Ala	Asn	Val	Ile	Ser	Pro	Ile	Ala	Asn
1105					1110					1115				1120	
Ala	Asp	Val	Val	Lys	Asn	Thr	Asn	Val	Val	Val	Ser	Gly	Leu	Asp	Arg
				1125					1130					1135	
Ile	Thr	Glu	Thr	Ile	Asn	Phe	Phe	Ser	Phe	Leu	Ser	Gln	Ile	Lys	Thr
			1140					1145					1150		
Met	Asn	Glu	Asn	Ile	Glu	Glu	Tyr	Leu	Arg	Arg	Tyr	Arg	Leu	Gly	Glu
		1155					1160					1165			
Gly	Leu	Asp	Lys	Lys	Glu	Leu	Asp	Asn	Phe	Val	Tyr	Pro	Asn	Ile	Ala
	1170					1175					1180				
Ala	Ile	Val	Lys	Arg	Glu	Leu	Gly	Val	Ser	Gly	Ser	Ala	Leu	Ser	Ser
1185					1190					1195				1200	
Asn	Leu	Asp	Thr	Asp	Arg	Pro	Ile	Thr	Ile	Asp	Leu	Asn	Thr	Glu	Gln

				1205					1210				1215			
Pro	Leu	Ile	Val	Lys	Ala	Ser	Lys	Gly	Tyr	Asn	Arg	Tyr	Ala	Lys	Leu	
			1220					1225					1230			
Phe	Asn	Lys	Thr	Thr	Arg	Thr	Ala	Ala	Glu	Gln	Ala	Gln	Met	Glu	Gln	
		1235					1240					1245				
Tyr	Asn	Ala	Gln	Met	Ala	Ala	Asn	Thr	Ile	Pro	Gln	Leu	Val	Asn	Arg	
	1250					1255				1260						
Leu	Thr	Ile	Pro	Gly	Ser	Ile	Thr	Ala	Asp	Thr	Ala	Ile	Asn	Val	Val	
1265				1270					1275						1280	
Lys	Ala	Phe	Thr	Glu	Asn	Gly	Glu	Phe	Ser	Asn	Ala	Glu	Thr	His	Leu	
			1285					1290						1295		
Gly	Val	Met	Gly	Asn	Ala	Ile	Asn	Glu	Met	Gln	Pro	Leu	Phe	Thr	Asp	
			1300					1305					1310			
Gly	Phe	Asn	Val	Ala	Asn	Lys	Arg	Leu	Thr	Val	Asn	Val	Gly	Ser	Val	
	1315					1320					1325					
Ser	Lys	Leu	Ile	Gln	Asn	Gly	Leu	Thr	Val	Ser	Leu	Ile	Leu	Ala	His	
	1330				1335					1340						
Ser	Lys	Asp	Tyr	Val	Phe	Lys	Pro	Leu	Val	Gln	Asp	Phe	Ala	Lys	Leu	
1345				1350					1355						1360	
Leu	Leu	Ala	Val	Thr	Ala	Glu	Thr	Ser	Leu	Val	Val	Ser	Arg	Ser	Gln	
			1365					1370						1375		
Lys	Ser	Phe	Phe	Pro	Ile	Pro	Pro	Ser	Val	Phe	Ser	Ser	Gly	Gly	Leu	
			1380					1385					1390			
Phe	Lys	Ile	Asp	Arg	Glu	Met	Phe	Asp	Asn	Met	Lys	Thr	Asp	Tyr	Val	
		1395					1400					1405				
Val	Glu	Val	Ile	Arg	Gln	Leu	Ser	Lys	Asn	Ala	Thr	Ala	Ala	Ile	Glu	
	1410				1415					1420						
Arg	Cys	Asn	Asp	Ser	Asp	Ser	Ala	Ala	Arg	Ile	Ala	Lys	Ser	Gly	Glu	
1425				1430					1435					1440		
Ile	Tyr	Asn	Lys	Asp	Val	Ala	Ser	Thr	Thr	Ala	Ala	Pro	Gly	Thr	Ser	
			1445					1450					1455			
Ser	Ser	Ala	Leu	Thr	Leu	Phe	Ala	Asn	Asn	Leu	Gln	Asn	Pro	Ala	Lys	
		1460						1465				1470				
Val	Trp	Ser	Met	Gly	Ala	Leu	Pro	His	Phe	Asp	Met	Ala	Val	Val	Pro	
	1475					1480					1485					
Lys	Leu	His	Gly	Ile	Ser	His	Asp	Gln	Met	Phe	Arg	Leu	Ser	Thr	Tyr	
	1490					1495				1500						
Tyr	Gln	Gly	Ile	His	Lys	Met	Glu	Leu	Asn	Ser	Asp	Cys	Lys	Pro	Glu	
1505				1510					1515					1520		
Glu	Trp	Asp	Asn	Ser	Leu	Pro	Gly	Asn	Arg	Ala	Ser	Lys	Phe	Phe	Gly	

Val Met Ser Lys Glu Glu Asp Val Arg Ser Ser Ser Arg Lys Ile Met
1700 1705 1710
Gly Met Val Glu Gln Glu Ser Pro Val Met Gln Asp Ile Gly Ile Asp
1715 1720 1725
Arg Ile Ala Ser Leu Val Ser Thr Val Ala Thr Pro Lys Gln His Arg
1730 1735 1740
Arg Phe Leu Gln Thr Val Asn Asp Tyr Lys Asn Tyr Leu Ile Arg Lys
1745 1750 1755 1760
Val Asn Pro Leu Leu Ser Ser Arg Leu Gly Gly Ile Ser Pro Thr Ser
1765 1770 1775
Gly Asn Thr Asp Tyr Asn Leu Lys Ala Val Tyr Asp Gly Val Val Ser
1780 1785 1790
Ser Ser Ser Ser Met Thr Pro Ser Ser Met Ser Val Ser Asp Arg Phe
1795 1800 1805
Trp Ser Gly Val Phe Ser Gln Cys Leu Glu Thr Gly Pro Ser Met Phe
1810 1815 1820
Ala Asp Ala Gly His Gly Gly Ser Asn Met Phe Gln Ile Thr Ala Pro
1825 1830 1835 1840
Lys Leu Tyr Gly Ser Arg Val Asn Thr Tyr Ala Ala Leu Ser Ser Gly
1845 1850 1855
Val Glu Arg Leu Arg Asp Ser Ile Ser Ser Ala Thr Gln Glu Arg Lys
1860 1865 1870
Asn Arg Ile Ala Lys Ser Ile Glu Ala Leu Glu Thr Phe Val Thr Asp
1875 1880 1885
Val Val Gly Gly Asp Thr Leu Asp Gln Leu Arg Lys Ala Gln Asn Met
1890 1895 1900
Tyr Asn Lys Leu Ser Asp Ile Thr Ser Asn Ser Ile Tyr Ser Asp Phe
1905 1910 1915 1920
Gly Asn Ile Asp Cys Ala Lys Ile Met Lys Asn Val Thr Ser Lys Lys
1925 1930 1935
Met Thr Ala Arg Gln Gln Ser Asp Thr Ile Leu Ser Ser Leu Leu His
1940 1945 1950
Glu Leu Ala Gly Leu Val His Lys Gln Gln Pro Gln Leu Ala Thr Gln
1955 1960 1965
Phe Ala Ser His Val Ile Lys Ala Lys Tyr Val Thr Asn Asp Leu Asn
1970 1975 1980
Asn Ile His Glu Lys Glu Thr Phe Ser Gln Leu Met Ala Val Ala Gly
1985 1990 1995 2000
Val Ala Asp Tyr Tyr Asn Val Ser Ala Ala Ala Met Cys Gln Arg Leu
2005 2010 2015
Val Ala Ser Asp Val Thr Met Phe Leu Gly Gly Thr Met Leu Gln Gln
2020 2025 2030
Gly Leu Phe Val Ser Phe Leu Leu Asn Asn Val Leu Phe Ser Gln Val
2035 2040 2045
Ser Asp Asn Ile Lys Met Asn Glu Leu Asn Asp Glu Thr Lys Ser Leu
2050 2055 2060
Leu Val Lys Leu Val Gly Phe Cys Gly Thr Val Ser Asp Ala Leu Gly
2065 2070 2075 2080
Ser Arg His Val Ser Ser Ile Arg Arg Val Gln Asn Glu Glu Asp Lys
2085 2090 2095
Lys Leu Asp Arg Ser Phe Val Thr Ser Lys Ala Tyr Arg Asp Leu Arg
2100 2105 2110
Lys Lys Thr Glu Leu Tyr Arg Glu Thr Asp Thr Ile Asn Lys Leu Phe
2115 2120 2125
Gly His Gln Asn Phe Met Ser Tyr Glu Ser Ser Met Leu Lys Arg Thr
2130 2135 2140
Ser Leu Val His Asp Ala Val Ser Gly Pro Arg Pro Arg Arg Tyr Ser
2145 2150 2155 2160
Thr Leu Glu Asp Val Leu Glu Ala Pro Ser Thr Val His Lys Ser Phe
2165 2170 2175
Met Val Ser Tyr Pro Glu Arg Ala Ala Ala Ser Arg Arg Val Lys Arg

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			2180					2185					2190		
Ala	Gly	Leu	Arg	Ala	Asp	Asn	Arg	Met	Glu	Ser	Leu	Tyr	Gly	Glu	Glu
		2195					2200					2205			
Val	Leu	Asn	Asp	Met	Arg	Ser	Ser	Ala	Val	Ser	Ser	Glu	Met	Met	Asp
	2210						2215				2220				
Ile	Glu	Tyr	Gly	Glu	Gly	Gly	Phe	Met	Met	Met	Ile	Ser	Asp	Asp	Glu
2225					2230					2235					2240
Asp	Asp	Ile	Ala	Phe	Ile	Asp	Ser	Glu	Glu	Glu	Ser	Glu	Ser	Ser	Thr
			2245					2250						2255	
Asp	Phe	Ser	Ser	Ser	Asp	Glu	Tyr	Ser	Asp	Ser	Ser	Asp	Glu	Tyr	Asp
		2260						2265					2270		
Phe	Asp	Asp	Asp	Asn	Asn	Gly	Gln	Ser	Pro	Tyr	Ser	Thr	Thr	Ser	Tyr
	2275						2280						2285		
Ser	Tyr	Asp	Ala	Leu	Asp	Arg	Leu	Asn	Ser	Ala	Ala	Lys	Pro	Leu	Thr
	2290					2295					2300				
Ala	Ile	Tyr	Gly	Cys	Arg	Gly	Glu	Gly	Glu	Asp	Asp	Glu	Glu	Asn	Asp
2305					2310					2315					2320
Leu	Tyr	Glu	Glu	Glu	Gln	Glu	Arg	Arg	Arg	Arg	Ser	Ser	Lys	Met	
			2325					2330						2335	
Gly	Lys	Ile	Leu	Arg	Asp	Leu	His	Glu	Ser	Asp	Asp	Asp	Asp	Asp	Asp
		2340						2345					2350		
Tyr	Phe	Asp	Asp	Glu	Phe	Asp	Gly	Glu	Arg	Ser	Met	Ser	Glu	Thr	Ile
	2355						2360					2365			
Ala	Thr	Arg	Arg	Ala	Gly	Arg	Ile	Gln	Tyr	Gly	Pro	Gly	Phe	Leu	Ser
	2370					2375					2380				
His	Ser	Asn	Ile	Leu	Asn	Arg	Pro	Ala	Lys	Ala	Arg	Ala	Phe	Leu	Thr
2385					2390					2395					2400
Arg	Gly	Lys	Lys	Phe	Arg	Pro	Ser	Ala	Tyr	Asp	Arg	Phe	Phe	Met	Glu
			2405						2410					2415	
Asp	Asp	Asp	Ser	Leu	Leu	Phe	Ser	Asp	Glu	Ser	Thr	Thr	Ser	Ser	Ser
		2420						2425					2430		
Ser	Ser	Asp	Ser	Pro	Phe	Ser	Ser	Phe	Ser	Lys	Gly	Arg	Lys	Cys	Lys
	2435						2440					2445			
Arg	Arg	Thr	Ser	Glu	Asp	Gln	Cys	Ala	Phe	Val	Lys	Arg	Val	Val	Arg
	2450					2455					2460				
Ala	Phe	Val	Pro	Thr	Arg	Val	Thr	Met	Ile	Asn	Gly	Arg	Val	Ser	Met
2465					2470					2475					2480
Ile	Thr	Pro	Val	Thr	Ser	Glu	Asn	Thr	Val	Gly	Phe	Tyr	Glu	Asn	Tyr
			2485					2490						2495	
Gln	Lys	Ala	Asn	Lys	Arg	Glu	Arg	Ala	Arg	Leu	Ile	Glu	Glu	Tyr	Lys
		2500						2505					2510		
Ile	Val	Lys	Gly	Ala	Ser	Ala	Thr	Leu	Pro	Asp	Glu	Tyr	Val	Glu	Gly
	2515						2520					2525			
Arg	Ala	Ser	Lys	Gln	Val	Ser	Pro	Arg	Glu	Leu	Arg	Arg	Ser	Leu	Ile
	2530					2535					2540				
Lys	Ala	Ala	Ala	Tyr	Val	Ala	Arg	Thr	Gln	Glu	Ser	Asn	Leu	Asn	Ile
2545					2550					2555					2560
Ile	Phe	Asp	Ala	Leu	Thr	Thr	Thr	Ser	Asn	Ala	Thr	Leu	Val	Asn	Asp
		2565						2570						2575	
Pro	Ser	Thr	Leu	Leu	Gly	Asp	Thr	Leu	Leu	Phe	Ala	Lys	Gln	Leu	Glu
		2580						2585					2590		
Ala	Ile	Thr	Glu	Arg	Arg	Asn	Arg	Leu	Met	Lys	Asp	Leu	Thr	Glu	Ile
	2595						2600					2605			
Ser	Pro	Ser	Leu	Phe	Thr	Ser	Phe	Gly	Asp	Ala	Ser	Lys	Asp	Thr	Gln
	2610					2615					2620				
Met	Met	Ala	Asp	Ala	Lys	Gln	Ile	Val	Ser	Gly	Gly	Asn	Phe	Lys	Ser
2625					2630					2635					2640
Ala	Gly	Tyr	Leu	Gly	Val	Pro	Leu	Arg	Thr	Leu	Ala	Ser	Cys	Ile	Lys
		2645						2650						2655	
Gly	Thr	Asn	Thr	Val	Asp	Arg	Leu	Leu	Ala	Thr	Lys	Asn	Lys	Asn	His
		2660						2665					2670		

Leu Glu Trp Met Thr Thr Ala Ala Ile Val Phe Ala Arg Ser Phe Asn
 2675 2680 2685
 Asp Thr Thr Phe His Ala Leu Glu Asp Thr Leu Lys Met Thr Ser Ala
 2690 2695 2700
 Leu Thr Asp Met Tyr Ser Ala Phe Thr Asn Leu Val Gly Ser Glu His
 2705 2710 2715 2720
 Ser Gln Arg Leu Lys Val Lys Ser Thr Leu Leu Asp Ser Ile Phe Asn
 2725 2730 2735
 Thr Arg Met Ala His Thr Glu Ala Val Met Gly Leu Val Tyr Pro Thr
 2740 2745 2750
 Ala Phe Ile Asn His Glu Met Pro Ser Asp Tyr Thr Gln Arg Arg Glu
 2755 2760 2765
 Met Gln Ser Leu Ala Leu Asn Ile Leu Arg Gly Val Asn Cys Ser Gln
 2770 2775 2780
 Leu Pro Arg Lys Asp Ile Gly Asp Thr Ala Gly Leu Leu Thr Phe Ile
 2785 2790 2795 2800
 Thr Ser Arg Lys Phe Ala Gly Tyr Gly Gly Glu Arg Gly Gly Leu Ser
 2805 2810 2815
 Leu Tyr Arg Met Ser Ile Val Asp Ala Leu Ser Cys Pro Ser Asp Asn
 2820 2825 2830
 Arg Leu Lys Gly Ala Val Ser Leu Glu Val Gly Lys Trp Gln Asp Met
 2835 2840 2845
 Gly Glu Glu Ile Phe Tyr Lys Arg Ser Asn Asp Leu Val Asp Phe Cys
 2850 2855 2860
 Ser Lys Asn Asn Ile Ser Leu Glu Asn Ala Val Gly Pro Ile Ala Arg
 2865 2870 2875 2880
 Phe Val Pro Asn Gly Thr Asn Met Ala Asp Ile Gly Met Thr Asp Ile
 2885 2890 2895
 Ile Ser Arg Thr Val Lys Asp Asp Ala Ser Met Ile Arg Leu Arg Arg
 2900 2905 2910
 Ala Glu Glu Gly Ala Gly Ala Ala Gly Lys Phe Ile Thr Ala Ser Ala
 2915 2920 2925
 Met Gly Asn Leu Tyr Gly Gly Ile Asp Thr Val Val Asn Leu Thr Glu
 2930 2935 2940
 Lys Leu Tyr Asp Ser Phe Val Leu Leu Gln Asp Ser Asp Ser Phe Asn
 2945 2950 2955 2960
 Thr Pro Thr Glu Met Ala Thr Ala Ile Ile Asn Arg Met Lys Ser Arg
 2965 2970 2975
 Lys His Lys Ala Leu Lys Thr Pro Phe Gly Gly Asp Ile Ala Thr Tyr
 2980 2985 2990
 Lys Asn Phe Pro Ser Ser Ser Glu Ala Ile Val Val Arg Ala Lys Glu
 2995 3000 3005
 Met Arg Asn Ser Ile Ser Thr Ile Val Met Asp Ile Ser Lys Ser Arg
 3010 3015 3020
 Gly Ile Asn Ser Phe Ser Ser Arg Ser Gly Ser Thr Leu Ala Lys Ile
 3025 3030 3035 3040
 Ser Thr Ser Glu Phe Glu Arg Ile Thr Ser Ala Val Leu Ser Asn Thr
 3045 3050 3055
 Lys Ala Asn Leu Arg Thr Ile Glu Asn Arg Leu Ala Glu His Tyr Asn
 3060 3065 3070
 Lys Leu Lys Gln Phe Ser His Asn Asp Gly Leu Ser Glu Thr Arg Ala
 3075 3080 3085
 Val Val Ala Val Ile Ala Glu Ser Leu Thr Pro Val Tyr Ala Asp Asp
 3090 3095 3100
 Thr Ser Gly Ala Ser Val Ser Glu Leu Leu Thr Asp Asn Thr Leu Leu
 3105 3110 3115 3120
 Lys Phe Ile Val Gln Asn Glu Leu Lys Asn Ile Glu Glu Ala Lys Arg
 3125 3130 3135
 His Val Thr Ala Ala Ile Glu Gly Ser Ser Gln Leu His Glu Lys Met
 3140 3145 3150
 Leu Ser Leu Leu Val Ala Ser Ala Asp Ile Asn Arg Met Ser Ala Gln

Ala Ile Asp Lys Leu Asn Glu Tyr Tyr Gln Leu Ile Asp Ala Ile Lys
 3650 3655 3660
 Thr Lys Ile Val Ser Asp Thr Lys Gln Ala Ser Ser Trp Ala Ile Lys
 3665 3670 3675 3680
 Glu Thr Asp Lys Glu Leu Asp Met Asp Lys Glu Gln Val Ile Ser Lys
 3685 3690 3695
 Ile Asn Asn Leu Gln Gln Asn Phe Ser Asn Glu Ser Asp Lys Ile Lys
 3700 3705 3710
 Met Ala Ile Ser Val Leu Asp Asn Lys Arg Asn Glu Leu Glu Leu Gln
 3715 3720 3725
 Asn Asn Lys Thr Arg Ser Phe Ile Glu Thr Thr Lys Ser Arg Ile Glu
 3730 3735 3740
 Ala Gly Gly Gly Asp Val Ala Asn Phe Lys Glu Ile Ile Asp Tyr Glu
 3745 3750 3755 3760
 Asn Thr Ser Glu Asn Asp Asn Asn Leu Phe Gln Ser Leu Lys Ala Phe
 3765 3770 3775
 Ala Ala Asp Asn Ser Gly Thr Val Tyr Thr Pro Thr Asp Met Ser Asn
 3780 3785 3790
 Gly Arg Asp Thr Lys Ser Asp Ser Lys Phe Val Asp Met Tyr Asn Lys
 3795 3800 3805
 Gln Ile Gly Gly Ile Lys Leu Ile Asn Glu Gly Gln Asn Thr Val Lys
 3810 3815 3820
 Val Asp Phe Ser Lys Ala Leu Glu Ala Phe Pro Arg Gln Ser Asn Gly
 3825 3830 3835 3840
 Ala Ser Glu Pro Val Ser Ser Ser Val Val Glu Arg Arg Gln Arg Glu
 3845 3850 3855
 Arg Leu Gln Ala Val Glu Met Phe Met Ala Ile Met Met Glu Arg Thr
 3860 3865 3870
 Glu Ser Leu Arg Lys Arg Leu Ala Asp Ser Ala Ala Gln Trp Asn Thr
 3875 3880 3885
 Val Asn Asn Val Glu Glu Thr Val Asn Ser Gly Met Val Asn Ile Lys
 3890 3895 3900
 Ser Leu Thr Glu Ile Arg Asn Gln Ala Gln Ile Ala Glu Ser Thr Ala
 3905 3910 3915 3920
 Leu Asn Ser Ile Asn Asp Glu Ile Val Glu Ser Pro Leu Thr Leu Ser
 3925 3930 3935
 Leu Gly Ala Arg Val Asp Gln Leu Leu Ile Lys Val Asp Arg Val Gly
 3940 3945 3950
 Ser Ile Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Pro
 3955 3960 3965
 Lys Leu Thr Ala Thr Glu Gln Arg Lys Glu Gln Gln Tyr Ala Ala Asp
 3970 3975 3980
 Arg Val Val Tyr Asp Pro Ser Tyr Thr Cys Phe Leu Gln Pro Leu His
 3985 3990 3995 4000
 Glu Thr Ile Lys Arg Ile Ser Ser Val Tyr Asn Ser Lys Asn Lys Gly
 4005 4010 4015
 Pro Leu Ser Asn Thr Arg Gly Val Pro Thr Ser Asp Ala Asp Leu Gln
 4020 4025 4030
 Leu Met Thr Ile Thr Asp Leu Ser Arg Ser Val Leu Asp Ser Ser Ser
 4035 4040 4045
 Thr Ser Ser Lys Lys Met Leu Tyr Glu Asn Val Pro Ser Ser Ile Val
 4050 4055 4060
 Pro Gly Leu Cys Gln Gln Cys Ala Met Met Ile Thr Asn Val His Glu
 4065 4070 4075 4080
 Ala Thr His Thr Ser Pro His Ser Phe Asn Phe Glu Asn Lys Arg Ser
 4085 4090 4095
 Leu Lys Gln Leu Thr Glu Met Leu Asn Ala Ala Thr Ser Ser Ser Asp
 4100 4105 4110
 Gly Pro Ala Val Arg His Asp Val Leu Thr Met Leu Glu Ser Asn Asn
 4115 4120 4125
 Gly Tyr Val Lys Asp Phe Gly Phe Thr Gln Lys Val Ala Cys Ile Thr

4130	4135	4140	
Pro Val Asn Thr Leu	Leu Gly Gly Thr Phe Ser Gly Asn Val Ala Pro		
4145	4150	4155	4160
Asn Thr Val Ile Leu	Pro Thr Ser Glu Leu Phe Asn Cys Pro Gly Val		
	4165	4170	4175
Glu Asn Asp Lys Phe Arg Ser Met Val Asn Arg Thr Thr Asp Lys Asn			
	4180	4185	4190
Val Ala Asp Ala Pro Lys Ser Ser Ala Ser Ile Val Glu Thr Leu Ala			
	4195	4200	4205
Arg Thr Ser Pro Asn Ala Glu His Leu Tyr Phe Pro Phe Lys Asp Gln			
	4210	4215	4220
Arg Arg His Phe Asn Ser Ile Thr Asp Ala Ile Ile Ser Gly Met Ser			
	4225	4230	4235
Gly Glu Ser Ser Ser Ser Glu Leu Asn Thr Thr Cys Asp Gln Asn Leu Val			
	4245	4250	4255
Asn Ile Asp Gln Thr Thr Gly Phe Pro Val Phe Thr Gly Arg Lys Gln			
	4260	4265	4270
Gly Glu Arg Arg Ile Val His Thr Glu Asn Thr Met Glu Gly Ala Arg			
	4275	4280	4285
Lys Asp Lys Asn Ser Gly Ile Pro Ser Cys Thr Lys Asp Arg Gln Thr			
	4290	4295	4300
Tyr Ile Asp Met Gly Thr Lys Phe Met Val Ala Pro Gly Ser Leu Leu			
	4305	4310	4315
Asn Ala Asn Lys Glu Glu Thr Leu Arg Leu Asn Arg Leu Ser Asp Ile			
	4325	4330	4335
Asn Asn Val Arg His Tyr Gly Thr Asp Val His Val Ala Gly Ala Asn			
	4340	4345	4350
Ser Ala Trp Arg Ile Gly Glu Val Val Arg Ala Ala Ser Ser Phe Pro			
	4355	4360	4365
Asp Gly Asp Lys Glu Ser Ala Met Lys Lys Met Leu Leu Leu Gly Ser			
	4370	4375	4380
Val Ser Ala Ile Ser Ala Gln Lys Ser Ala Ser His Ile Asn Asp Pro			
	4385	4390	4395
Thr Ala Leu Leu Ser Thr Asn Thr Ser Ile Gln Asn Leu Val Lys Glu			
	4405	4410	4415
Ala Phe Pro Asp Pro Val Cys Ser Ser Asn Tyr Leu Gly Ser Ala Glu			
	4420	4425	4430
Ser Thr Phe Ala Thr Gln Leu Ala Tyr Arg Gln Arg Leu Phe Pro Asn			
	4435	4440	4445
Gly Asp Asp Glu Asn Val Thr Thr Val Ser Asn Ile Cys Pro Met Asp			
	4450	4455	4460
Leu Met Gly Ser Thr Lys Arg Tyr Asn Asp Ala Phe Asn Asn Ile Phe			
	4465	4470	4475
Gly Ser Lys Met Thr Ser Thr Asn Lys Lys Gly Ser Asn Cys Glu Asn			
	4485	4490	4495
Leu Leu Lys Ser Ala Met Ser Asn Val Pro Ala Ile Asn Thr Ala Phe			
	4500	4505	4510
Gly Ala Phe Glu Glu Ala Ser Ser Ser Val Arg Asn Arg Leu Ser Pro			
	4515	4520	4525
Leu Tyr Glu Asp Ser Thr Lys Tyr Ser Ser Asn Gln Leu Ala Val Gln			
	4530	4535	4540
Ala Met Thr Asp Thr Ala Val Asp Ala Leu Ser Ala Val Ser Thr Val			
	4545	4550	4555
Val Gly Arg Gln Asn Gly Arg Asn Thr Leu Leu Ser Leu Pro Thr Ser			
	4565	4570	4575
Ile Thr Ser Ile Ala Thr Ser Gly Arg Pro Ser Leu Ser Tyr Ser Ser			
	4580	4585	4590
Asp Met Lys Ser Asn Leu Ile Lys Thr Ile Ser Arg Ile Asn Arg Asp			
	4595	4600	4605
Ala Ser Leu Leu Ser Met Gly Asp Ser Gln Val Ala Ala Gly Ser Ser			
	4610	4615	4620

Phe Phe Asn Ser Phe Leu Arg Ser Ser Ser Ile Pro Val Thr Thr Ser
 4625 4630 4635 4640
 Gln Asp Gly Asn Val Ala Ala Ala Glu Ile Val Leu Gly Thr Ile Leu
 4645 4650 4655
 Asp Lys Thr Val Glu Ile Asn Lys Arg Phe Glu Met Leu Gly Gly Gly
 4660 4665 4670
 Lys Met Val Ala Gly Ser Pro Glu Ala Arg Ala Ile Gln Arg Asn Thr
 4675 4680 4685
 Met Ser Ser Ile Leu Gln Met Asn Glu Asn Glu Leu Ala Arg Asp Leu
 4690 4695 4700
 Cys Glu Ile Glu Asn Lys Ile Glu Thr Arg Gln Leu Arg Asp Ala Phe
 4705 4710 4715 4720
 Gln Asp Leu Lys Arg Ser Met Leu Met Thr Pro Gly Gly Val Gly Ala
 4725 4730 4735
 Ile Ser Ser Gly Ala Ser Thr Asn Asn Val Pro Leu Ser Leu Leu Met
 4740 4745 4750
 Ser Arg Val Asp Ala Ser Ser Gly Leu Leu Met Asn Asn Asn Ser Ala
 4755 4760 4765
 Asn Val Met Glu Ala Val Asp Ser Phe Asn Thr Thr Pro Leu Leu Val
 4770 4775 4780
 Arg His Met Met Leu Asp Ser Gly Lys Ser Pro Val Pro Met Ala Lys
 4785 4790 4795 4800
 Glu Ile Arg Ser Met Leu Thr Gln Pro Arg Ala Leu Thr Ala Arg Ala
 4805 4810 4815
 Leu Leu Ser Glu Ser Ser Pro Leu Leu Thr Glu Ile Cys Leu Tyr Asn
 4820 4825 4830
 Thr Arg Asp Thr Gln Pro Glu Arg Ala Val Asp Arg Leu Leu Thr Ser
 4835 4840 4845
 Ala Tyr Leu Val Lys Gln Ala Lys Arg Phe Asp Gly Val Asp Pro Ala
 4850 4855 4860
 Phe Pro Ala Ala Leu Thr Cys Ala Ser His Leu Met Leu Ser Ser Met
 4865 4870 4875 4880
 Asp Ser His Thr Lys Ser Ser Phe Met Asp Asn Ile Lys Leu His Met
 4885 4890 4895
 Thr Asp Thr Gln Cys Phe Phe Lys Asn Ile Glu Arg Phe Glu Lys Phe
 4900 4905 4910
 Leu Gly Arg Tyr Gly Asp Glu Tyr Ala Met Ser His Lys Gln Asn Cys
 4915 4920 4925
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 4930 4935 4940
 His Leu Val Ser Ser Phe Ala Phe Ala Arg Pro Glu Val Ser Met Glu
 4945 4950 4955 4960
 Glu Ile Arg Ala Thr Pro Tyr Gln Ala Asn Lys Leu Ile Ser Asp Lys
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 His Tyr Val Met Asn Met Ser Lys Ile Asp Ser Arg Val Thr Gly Ser
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 Ser Leu Leu Lys Lys Val Ser Glu Trp Thr Glu Met Arg Met Asn Ser
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 Gly Met Thr Thr Ala Gly Val Asn Leu Asp Val Ile Val Lys Pro Asn
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 Pro Arg Asn Arg Tyr Ile Gln Lys Ser Thr Met Asn Ala Gln Thr Val
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Val Tyr Glu Asn	Thr Lys Glu Met	Ile Asp Arg Leu	Gly Ser Asp Asp			
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Asp Ser Glu Thr	Thr Ser Asn Asn	Gly Pro Val Leu	Ile Ser Glu Ala			
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Met Lys Asn Ala	Val Tyr His Thr	Leu Ile Ser Gly	Lys Ala Ala Arg			
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Pro Glu Asn Val	Pro Phe Ala Ser	Cys Ala Ser Gly	Pro Leu Ala Phe			
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Asp Phe Leu Leu	Ser Lys Gly Asp	Thr Phe Glu Glu	Lys Asn Ala Glu			
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Gln Gly Ala Ala	Ala Ala Val Ser	Ser Thr Tyr Ser	Ser Ser Ser Asn			
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Thr Thr Leu Arg	Lys His Leu Ala	Arg Val Phe Glu	Ala Ile Ser Lys			
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Gln Val Thr Asp	Ala Glu Phe Lys	Asp Ile Leu Asn	Asp Ile Glu Arg			
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Asn Ile Ser Ser	Asp Tyr Thr Asn	Cys Pro Pro Asn	Thr Asn Gln Asn			
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Ala Phe Ala Ile	Lys Arg Glu Phe	Ser Arg Ile Val	Ser Phe Leu Thr			
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Ile Leu Arg Lys	Asn Ile Thr Pro	Ala Leu Val Asp	Pro Lys Gly Ala			
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Leu His Glu Lys	Val Ala Ile Tyr	Leu Thr Leu Leu	Ser Thr Lys Ser			
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Lys Leu Glu Asn	Phe Phe Gln Tyr	Gly Leu Ser Asn	Ser Ser Ser Val			
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Asp Leu Ser His	Leu Lys Pro Ile	Asn Cys Ser Asn	Asn Val Lys Asn			
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Ile Glu Asp Thr	Phe Met Tyr Arg	Asn Val His Pro	Ile Leu Ile Met			
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Ala Leu Pro Glu	Asn Phe Thr Ala	Leu Leu Gln Gln	Glu Gln Met Asp			
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Pro Asp Thr Ala	Ile Glu Ser Arg	Arg Ser Leu Thr	Thr Phe Leu Asn			
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His Pro Asn Thr	Ala Ser Met Ala	Asn Gly Ala Arg	Ala Ala Val Gly			
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Ala Gly Gly Gly	Asn Pro Met Gly	Leu Ser Ser His	Ile Leu His Glu			
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Ser Thr Val Thr	Ser Asn Pro Val	Thr Thr Thr Glu	Asn Val Val			
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Asn Tyr His Ser	Ser Val Thr Gln	Asp Pro Val Met	Val Val Asn Pro			
	5475		5480			5485
Phe Lys Asp Ser	Ala Arg Leu Ile	Val Asn Asn Asn	Asn Thr Gly Ile			
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Asp Val Leu Asn	Asp Lys Ser Cys	Asn Tyr Leu Gln	Val Ser Met Pro			
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Ser Ser Ser Ser	Ser Asp Thr Phe	Lys Tyr Val Arg	Arg Asp Asn Thr			
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Pro Val Asn Leu	Pro Arg Val Thr	Pro Ala Val Leu	Cys Ser Asp Ala			
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Ser Ser Asn Leu	Leu Asp Val Phe	Ser Arg Ala Asp	Ile Val Leu Glu			
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Asn Met Asn Val	Arg Phe Gly Phe	Met Pro Glu Ile	Ile Ala Ala Val			
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 Lys Lys Thr Thr Val Asp Pro Val Thr Gly Asp Ile Val Ile Thr Asn
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 Ser Phe Lys Trp Gly Asp Ile Asn Asp Arg Lys Met His Ala Lys Ala
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 Phe Pro Thr Phe Phe Ile Gly Asn Pro Thr Ala Ala Ala Thr Ala Asn
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 Gly Val Pro Leu Thr Ser Glu Gly Ile Ser Leu Thr Glu Glu Lys Arg
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 Lys Lys Ile Ala Gly Ile Ser Glu Gly Ser Ile Gly Thr Gly Ala Leu
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 Lys Gly Trp Asn Asn Ile Val Gln Leu Gln Gln Thr Phe Lys Lys Ala
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 Ser Asp Lys Leu Thr His Leu Leu Arg Ser Gly Gly Ile Pro Pro Arg
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 Ser Gln Glu Thr Asn Ala Ile Ile Asn Lys Met His Asp Ser Phe Lys
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 Thr Leu Leu Leu Asp Ser Asp Ser Ile Ser Asn Leu Tyr Asn Thr Asp
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 Tyr Ser Ala Arg Gln Leu Thr Asp Leu Ile Thr Val Pro Glu Tyr Gly
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 Lys Asn Ala Pro Val Ser Ala Gln Glu Met Ala Cys Ala Ser Leu Thr
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<211> 2190

<212> DNA

<213> SHRIMP

<400> 62

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<212> PRT

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Lys Glu Glu Asp Ala Gly Ile Glu Ile Glu Thr Arg Val Val Val Phe
35          40          45
Ser Arg Cys Val Ser Val Gln Glu Leu His Thr Ile Asn Pro Asn Asp
50          55          60
Glu Gly Phe Ser Val Gln Leu Phe Lys Asp Tyr Leu Lys Leu Gln Ser
65          70          75          80
Ala Gln Gly Lys Lys Pro Ile Gly Ile Gln Ile Lys Ala Gly Glu Asp
85          90          95
Leu Glu Arg Arg Leu Ile Ser Gly Gly Thr Ala Tyr Leu Asp Pro Ala
100          105          110
Thr His Leu Phe Tyr Leu Asp Phe Ser Leu Tyr Pro Asn Tyr Ser Ile
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WO 01/38351

PCT/US00/28888

157

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Val	Leu	Ile	Arg	Val	Thr	Phe	Ser	Thr	His	Glu	Lys	Ala	Ile	Glu	Ala
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Ala	Ile	Lys	Lys	Ile	Met	Leu	Arg	Lys	Val	Phe	Phe	Lys	Asp	Gly	Asp
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Leu	Asp	Phe	Gly	Tyr	Leu	Arg	Ile	Pro	Lys	Ser	Lys	Leu	Asp	Lys	Phe
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Thr	Pro	Tyr	Phe	Arg	Ser	Gln	Tyr	Gly	Ile	Val	Asn	Val	Glu	Lys	Asn
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Ser	Arg	Trp	Tyr	Leu	Tyr	Asn	Thr	Asp	Ser	Glu	Trp	Glu	Tyr	Lys	Asn
				245					250					255	
Val	Ala	Glu	Glu	Arg	Val	Gly	Pro	Arg	Gln	Leu	Val	Lys	Lys	Tyr	Gly
			260					265					270		
Ala	Lys	Cys	Glu	Asn	Leu	Cys	Phe	Arg	Asp	Ile	Asp	Leu	Arg	Lys	Lys
	275						280					285			
Glu	Ala	Lys	Glu	Lys	Arg	Asp	Ile	Glu	Arg	Glu	Thr	Glu	Ser	Arg	Tyr
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Val	Val	Val	Thr	Leu	Thr	His	Lys	His	Glu	Met	Pro	Glu	Asn	Met	Pro
305					310					315					320
Tyr	Phe	Gly	Pro	Lys	Cys	Ser	Val	Val	Arg	Leu	Asp	Glu	Thr	Arg	Ile
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Leu	Leu	Cys	Phe	Val	Asp	Glu	Ile	Ser	Tyr	Asn	Asp	Glu	Asp	Val	Asp
			340					345					350		
Glu	Ile	Leu	Ser	Glu	Asn	Arg	Ser	Leu	Arg	Asn	Val	Ser	Ile	Arg	His
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Lys	Glu	Asn	Val	Pro	Val	His	Thr	Leu	Leu	Lys	Lys	Gly	Val	Ser	Ile
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His	Ala	Arg	Phe	Thr	Leu	Asn	Gly	Leu	Asp	Asp	Ala	Leu	Ile	Ile	Leu
385					390					395					400
Lys	Arg	Ile	Pro	Lys	Thr	Tyr	Phe	Glu	Asp	Glu	Glu	Leu	Gln	Ala	Ala
				405					410					415	
Cys	Ala	His	Val	Asn	Leu	Glu	Gln	Tyr	Glu	Trp	Leu	Cys	Ser	Asn	Asn
			420					425					430		
Arg	Gly	Asn	Lys	Val	Glu	His	Val	Lys	Ser	Arg	Val	Val	Thr	Arg	Ala
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Val	Lys	Arg	Arg	Arg	Lys	Cys	Arg	His	Trp	Ile	Tyr	Phe	Asp	Lys	Asp
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Thr	Leu	Asn	Leu	Asn	Tyr	Lys	Tyr	Phe	Asp	Lys	Lys	Val	Thr	Ala	Ser
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Met	Ala	Ser	Lys	Ile	Cys	Asn	Ala	Lys	His	Asp	Cys	Leu	Val	Phe	His
				485					490					495	
Arg	Lys	Met	Glu	Leu	Glu	Asp	Leu	Thr	Glu	Ser	Ala	Tyr	Phe	Lys	Val
			500					505					510		
Glu	Pro	Ser	Pro	Ile	Asn	Phe	Ala	Lys	Leu	Lys	Ser	Cys	Pro	Asp	Val
			515				520					525			
Lys	Tyr	Val	Gln	Lys	Lys	Thr	Asp	Gly	Thr	Phe	Ser	Val	Ile	Arg	Phe
	530					535					540				
Phe	Arg	Asn	Met	Thr	Lys	Gly	Asp	Leu	Ile	Gln	Arg	Met	Asp	Leu	Phe
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Cys	Arg	Phe	Ile	Pro	Asp	Ser	His	Thr	Ile	Thr	Leu	Leu	Ser	Arg	Ala
				565					570					575	
Asp	Phe	Tyr	Ala	Cys	Lys	Arg	Gly	Glu	Ser	Met	His	Met	Cys	Thr	Asn
			580					585					590		
Lys	His	Arg	Ile	Leu	His	Tyr	Lys	Phe	Ser	Asn	Ala	Pro	His	Ala	Ala
			595				600					605			
Ile	Glu	Gln	Ile	Thr	Asn	Ile	Ile	Ser	Asp	Thr	Arg	Gly	Arg	Lys	Gly

610 615 620
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 625 630 635 640
 Asp Gly Arg Arg Tyr Glu Ala Lys Tyr Thr Gly Thr Leu Thr Glu Tyr
 645 650 655
 Lys Arg Asn Glu Asp Lys Thr Phe Lys Ser Leu Leu Ala Pro His Leu
 660 665 670
 Thr Pro Val Asn Lys Pro Tyr Asn Ile Asn His Leu Tyr Glu Gln Tyr
 675 680 685
 Gly Asn Phe Asp Glu Glu Leu Glu Asp Lys Leu Arg Ser Gly Phe Ile
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 35 40 45
 Leu Pro Asn Ser Leu Pro Phe Thr Arg Ser Pro Asn Thr Thr Cys Gly
 50 55 60
 Ser Arg Glu Ala Ala Asn Ala Thr Glu His Phe Ile Thr Val Phe Ala
 65 70 75 80
 Lys Asp Lys Tyr Glu Arg Lys Arg Val Lys Arg Thr Ile Gly Phe Thr
 85 90 95
 Leu Asp Asn Thr Lys Glu Leu Thr Pro Asn Arg Tyr Leu Val Ala Asp
 100 105 110

Val Tyr Ser Trp Gln Glu Glu Lys Met Val Phe Glu Gly Phe Cys Val
 115 120 125
 Pro Pro Gly Lys Ser Gly Thr Phe Val Arg Tyr Ser Asn Glu Asp Lys
 130 135 140
 Ser Phe Leu Leu Ala Asp Thr Gly Arg Tyr Met Lys Lys Lys Tyr Asp
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 Asp Pro Glu Asn Lys Thr Ser Ser Gly Gly Asp Asp Asp Asp Asp
 165 170 175
 Asp Asp Asp Asp Asp Asp Asn Asn Asn Val Asp Val Tyr Glu Glu Asn
 180 185 190
 Asp Pro Arg Asn Val Phe Glu Val Glu Lys Asp Glu Lys Tyr Ala Cys
 195 200 205
 Thr Phe Ser Ile Leu Val Tyr Arg Ala Met Lys Lys Ser Pro Pro Val
 210 215 220
 Cys Arg Gly Leu Leu Val Glu Thr Asp Gly Pro Ser Ser His Pro Lys
 225 230 235 240
 Arg Ala Pro Ser Ala Phe Asn Pro Phe Gly Gly Ser Ser Met Leu Asn
 245 250 255
 Gly Tyr Gly Ala Gly Ala Asp Ala Leu Glu Glu Glu Asp Glu Val Asp
 260 265 270
 Gly Val Pro Glu Arg Glu Arg Ile Thr Asn Phe Ala Leu Lys Arg Gly
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 35          40          45
His Ser Leu Glu Thr Arg Tyr Gly Cys Gly Thr Gly Thr Ile Val Thr
 50          55          60
His Ala Gly Glu Val Ile Glu Gly Cys Thr Thr Val Ser Ser Ile Lys
 65          70          75          80
Glu Leu Ile Ser Val Leu Pro Glu Val Val Asp Val Ile Leu Ile Asp
 85          90          95
Glu Gly Gln Phe Phe Thr Asp Leu Val Leu Val Asn Arg Leu Ala Asp
100          105          110
Lys Gly Lys Arg Ile Val Ile Ala Ala Leu Asp Gly Thr Ser Asp Gln
115          120          125
Gln Met Phe Ser Pro Ile His Lys Leu Leu Pro Tyr Thr Asn Ser Ile
130          135          140
Val Lys Leu Ala Ser Lys Cys Met Ile Cys Lys Ile Asp Thr Lys Glu
145          150          155          160
Ala Pro Phe Thr Val Arg Phe Gly Asn Asp Asn Asp Asn Asn Val Ile
165          170          175
Cys Val Gly Gly Ala Glu Met Tyr Ala Ala Ala Cys Arg Asp Cys Tyr
180          185          190
Lys Lys Ile Asn Lys Lys Lys Asn Lys Gly Lys Leu Val Val Leu Glu
195          200          205
Gly Gly Asp Arg Cys Gly Lys Ser Thr Gln Ala Lys Leu Leu Leu Thr
210          215          220
Asn Lys Asn Ser Pro Leu Tyr Gly Gly Glu Tyr Met Cys Phe Pro Asp
225          230          235          240
Arg Ser Ser His Thr Gly Lys Leu Ile Asn Asp Tyr Leu Thr Lys Lys
245          250          255
Ile Glu Leu Asp Asp His Ala Ala His Leu Leu Phe Ser Ala Asn Arg
260          265          270
Trp Glu Val Cys Ser Lys Ile Lys Gln Leu Leu Asp Asp Gly Ile His
275          280          285
Val Val Met Asp Arg Tyr Tyr Tyr Ser Gly Ile Val Phe Ser Leu Arg
290          295          300
Val Asp Thr Val Glu Trp Cys Ser Ala Ser Asp Glu Gly Leu Pro Gln
305          310          315          320
Pro Asp Leu Val Leu Met Leu Leu Asp Val Glu Lys Cys Ser Asn
325          330          335
Arg Asp Thr Phe Gly Val Glu Arg Phe Glu Thr Asn Ser Ile Gln Glu
340          345          350
Arg Ala Arg Ala Leu Phe Leu Asp Leu Ala Asn Lys Asp Glu Lys Asn
355          360          365
Val Trp Ile Lys Val Asp Arg Thr Ile Glu Glu Val Gln Thr Lys Ile
370          375          380
Ile Asn Ile Val Tyr Asn Ile Val Glu Glu
385          390

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<210> 68

<211> 486

<212> DNA

<213> SHRIMP

<400> 68

atgttaccta gaaagacttt gcccgacact gaaaatgggt atttgtctt ggacgagtct 60

WO 01/38351

PCT/US00/28888

161

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cttctggaga aggtgtacta tgataacaac aatgaactga ttgtaagagt tgggtgggatt 120
tatatgcaga tatgcaagtc aaaatacatc ttccatcacg atgatccaga gaggttcttt 180
tatagtgtgt tggaggatta tcaccccatc aaagagattg ttgaacgact agcagaagag 240
gatggggtat ttttaggacc gtgggagttt ttatcgcgca aacaagtga cctccaacac 300
gggtgctaca aagctctttt gtcattgcc aaggacaaat attgtaacct attattacc 360
cagcaaatga aaaccaacct ggaaaaaatg gaagaaatac agcgtactag actcattcac 420
tctagaacgt acaatacacc ccagatagaa ttgtctgacc agctagatgg atgtgttata 480
tgtaa                                           486

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<210> 69
 <211> 161
 <212> PRT
 <213> SHRIMP

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<400> 69
Met Leu Pro Arg Lys Thr Leu Pro Asp Thr Glu Asn Gly Tyr Phe Val
 1           5           10           15
Leu Asp Glu Ser Leu Leu Glu Lys Val Tyr Tyr Asp Asn Asn Asn Glu
      20           25           30
Leu Ile Val Arg Val Gly Gly Ile Tyr Met Gln Ile Cys Lys Ser Lys
      35           40           45
Tyr Ile Phe His His Asp Asp Pro Glu Arg Phe Phe Tyr Ser Val Leu
      50           55           60
Glu Asp Tyr His Pro Ile Lys Glu Ile Val Glu Arg Leu Ala Glu Glu
      65           70           75           80
Asp Gly Val Phe Leu Gly Pro Trp Glu Phe Leu Ser Arg Lys Gln Val
      85           90           95
Asn Leu Gln His Gly Cys Tyr Lys Ala Leu Leu Ser Leu Pro Glu Asp
      100          105          110
Lys Tyr Cys Asn Leu Leu Leu Pro Gln Gln Met Lys Thr Asn Leu Glu
      115          120          125
Lys Met Glu Glu Ile Gln Arg Thr Arg Leu Ile His Ser Arg Thr Tyr
      130          135          140
Asn Thr Pro Gln Ile Glu Leu Ser Asp Gln Leu Asp Gly Cys Val Ile
      145          150          155          160
Cys

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<210> 70
 <211> 1926
 <212> DNA
 <213> SHRIMP

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<400> 70
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acaaactttc ttgaagctca caagcttgct gtggaacttc ttctcccgtc ctacagtagt 120
gatgtagttt attgtgactc tgagacgtac accaaaccta taccgatttt tgggaacaag 180
agtatagttt ctaccattgg agactatgtc ttatcaaacc ccaatgaaga tgtgagttac 240
caaatggttt cttccgtctt agaaaaattt cccttgctat tccactgcac ttataagacg 300
aatgaagaag ataaagggtat tcctctgtgg aagaagttgt acaacaaaag aaaattcaaa 360
ctcctcaact cattgttggt tcataacaac aagaactgga ctctgttcc agctatcccg 420
tttgacaggg agaatatatg tgatgcttca ggaaggagt ttcttatgag tgaaataatg 480
tccacgtcaa cttttcagac aatttgcaaa aacaacacac attacttgtt tgatatgtta 540
aatatggaac gtggcaaaca aggaggagt tttcttcact tctttgcatc taggaagaat 600
tcttttacta actttgaaa tgaagaaatg gactctcatg tgctcagtaa catagcgaaa 660
ttcatatgca atgaaaagga aaaactagac tctttcatac ctgccaacg aaaaatacca 720
tgccctgata aaactaatga tgaagggtac atcccgtgg aaatagcaat tatggaagac 780
aattaccctg cattgttata tctcgtttgt aggtatggag catcttgggc aaacacatac 840
ggggatcata atgaatctct caaagcgttt gcaataagaa atgatgcaaa agattgtctg 900
gaaattatag agtttataag tgatcactac agtttcaaca aaaatgtgac gaaggaagaa 960

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tttggttaaag agaagactgt agaatgtgtt ggatgtttat atgatattga agacgagaaa 1020
cgttgtttaca aactcccatg tggacatttc atgcatacat ttgcttgtc taataagtgt 1080
tctaaagcta acttttagatg tggttaaagt ttccaaacct ttgatgacac aatttttaga 1140
aaatgtcccc caactataca atggaaaatg ggtataaacc aaacgactaa ccataaggaa 1200
atggatttgt tcaatcgtgc atttgacaca tatttagatt ttatttgctc atataacgctc 1260
aaattagaca aaaaatcaaa acctaaacac aaacctgaaa acaaaaaggt ggaagaagaa 1320
ctagcaaaaa ggacagcaga aattgaagag gccataaaga aaaaggaaga agaactagca 1380
aaaaggacag cagaaattga agaggccata aagaaaaagg aagaagaact agcaaaaagg 1440
acagcagaaa ttgaagaggc catgaagaaa aaggaagaag aagaactctc aaaatataat 1500
aaaataattg aaaagggaaa aagacgactg aatgaagaat gtgtcaagct gagagatatt 1560
tcaactgcag ccataaacat gtacaaagag aaagtgaaga ttaatggtgt attactaaaa 1620
gattccgatc aggagtgtgc tgaggcgaaa gagagggtga ggaaaatttt attgctagaa 1680
gaagaacaaa aacttgacag atttttgttt agaccgaaac gagtagaaga acgtatattc 1740
ctaactaaaag atgatgaaac gttagccttc aagttagccc tagaaaagaa aacggaggac 1800
ataattgcga agaaaaacaa ccaaaaaggc agtgaaagaa gagatggaga atatactata 1860
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gaataa                                     1926

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<210> 71
<211> 637
<212> PRT
<213> SHRIMP

<400> 71

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Met Val Ala Ser Thr Pro Cys Pro Gly Pro Gly Pro Val Pro Thr Gln
1          5          10          15
Glu Leu Leu Ser Thr Asn Phe Leu Glu Ala His Lys Leu Val Val Glu
20         25         30
Leu Leu Leu Pro Ser Tyr Ser Ser Asp Val Val Tyr Cys Asp Ser Glu
35         40         45
Thr Tyr Thr Lys Pro Ile Pro Ile Phe Gly Asn Lys Ser Ile Val Ser
50         55         60
Thr Ile Gly Asp Tyr Val Leu Ser Asn Pro Asn Glu Asp Val Ser Tyr
65         70         75         80
Gln Met Val Ser Ser Val Leu Glu Lys Phe Pro Leu Leu Phe His Cys
85         90         95
Thr Tyr Lys Thr Asn Glu Glu Asp Lys Gly Ile Pro Leu Trp Lys Lys
100        105        110
Leu Tyr Asn Lys Arg Lys Phe Lys Leu Leu Asn Ser Leu Leu Val His
115        120        125
Asn Asn Lys Asn Trp Thr Pro Val Pro Ala Ile Pro Phe Asp Arg Glu
130        135        140
Asn Ile Cys Asp Ala Ser Gly Arg Ser Val Leu Met Ser Glu Ile Met
145        150        155        160
Ser Thr Ser Thr Phe Gln Thr Ile Cys Lys Asn Asn Thr His Tyr Leu
165        170        175
Phe Asp Met Leu Asn Met Glu Arg Gly Lys Gln Gly Gly Ser Phe Leu
180        185        190
His Phe Phe Ala Ser Arg Lys Asn Ser Phe Thr Asn Phe Glu Asn Glu
195        200        205
Glu Met Asp Ser His Val Leu Ser Asn Ile Ala Lys Phe Ile Cys Asn
210        215        220
Glu Lys Glu Lys Leu Asp Ser Phe Ile Pro Ala Asn Gly Lys Ile Pro
225        230        235        240
Cys Pro Asp Lys Thr Asn Asp Glu Gly Tyr Ile Pro Leu Glu Ile Ala
245        250        255
Ile Met Glu Asp Asn Tyr Pro Ala Leu Leu Tyr Leu Val Cys Arg Tyr
260        265        270
Gly Ala Ser Trp Ala Asn Thr Tyr Gly Asp His Asn Glu Ser Leu Lys
275        280        285
Ala Phe Ala Ile Arg Asn Asp Ala Lys Asp Cys Leu Glu Ile Ile Glu

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290		295		300
Phe Ile Ser Asp His Tyr	Ser Phe Asn Lys Asn	Val Thr Lys Glu Glu		
305	310	315	320	
Phe Val Lys Glu Lys Thr	Val Glu Cys Val Gly Cys	Leu Tyr Asp Ile		
	325	330	335	
Glu Asp Glu Lys Arg Cys Tyr	Lys Leu Pro Cys Gly His	Phe Met His		
	340	345	350	
Thr Phe Cys Leu Ser Asn Lys	Cys Ser Lys Ala Asn Phe	Arg Cys Val		
	355	360	365	
Lys Cys Phe Gln Thr Phe Asp	Asp Thr Ile Phe Arg Lys	Cys Pro Pro		
	370	375	380	
Thr Ile Gln Trp Lys Met Gly	Ile Asn Gln Thr Thr Asn	His Lys Glu		
385	390	395	400	
Met Asp Leu Phe Asn Arg Ala	Phe Asp Thr Tyr Leu Asp	Phe Ile Cys		
	405	410	415	
Ser Tyr Asn Val Lys Leu Asp	Lys Lys Ser Lys Pro Lys	His Lys Pro		
	420	425	430	
Glu Asn Lys Lys Val Glu Glu	Glu Leu Ala Lys Arg Thr	Ala Glu Ile		
	435	440	445	
Glu Glu Ala Ile Lys Lys Lys	Glu Glu Glu Leu Ala Lys	Arg Thr Ala		
	450	455	460	
Glu Ile Glu Glu Ala Ile Lys	Lys Lys Lys Glu Glu Glu	Leu Ala Lys Arg		
465	470	475	480	
Thr Ala Glu Ile Glu Glu Ala	Met Lys Lys Glu Glu Glu	Glu Glu Leu		
	485	490	495	
Ser Lys Tyr Asn Lys Ile Ile	Glu Lys Gly Lys Arg Arg	Leu Asn Glu		
	500	505	510	
Glu Cys Val Lys Leu Arg Asp	Ile Ser Thr Ala Ala Ile	Asn Met Tyr		
	515	520	525	
Lys Glu Lys Val Arg Ile Asn	Gly Val Leu Leu Lys Asp	Ser Asp Gln		
	530	535	540	
Glu Leu Ala Glu Ala Lys Glu	Arg Leu Arg Lys Ile Leu	Leu Leu Glu		
545	550	555	560	
Glu Glu Thr Lys Leu Asp Arg	Phe Leu Phe Arg Pro Lys	Arg Val Glu		
	565	570	575	
Glu Arg Ile Phe Leu Thr Lys	Asp Asp Glu Thr Leu Ala	Phe Lys Leu		
	580	585	590	
Ala Leu Glu Lys Lys Thr Glu	Asp Ile Ile Ala Lys Lys	Asn Asn Gln		
	595	600	605	
Lys Gly Ser Arg Asp Gly Glu	Tyr Thr Ile Thr Ser His	Ile Glu Lys		
	610	615	620	
Leu Pro Gln Ser Thr Ala Ser	Val Cys Val Leu Asn Glu			
625	630	635		

<210> 72

<211> 780

<212> DNA

<213> SHRIMP

<400> 72

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ccattcgacc tcgtccatac acgtcaagag tgtgataaaa agagagagca agactactca 120
tttttcatta ctgaaacgtg taaaggagag aatatttgta tacattcgta tgaacacacg 180
tcaaagatta ttgacacggg taataatgat tctacctcaa tagaggaact agaagtactg 240
aatatataca aagctataaa ccatttagaa aatatacctaa aactcaacaa aggagaaaaa 300
attatactga tggatgtaga aacaatgata ctggaaactc ataaaaatattt aatgaaaggg 360
attcttccca agggtaaaaa tggaagtttc agtacatgcg tacgctttgc tgtaaataag 420
aacaatgaac ggcattacta ccctgtatatt gaaacagaga aagaagcgtt caattctata 480
caaaatctag tagattatta taatgaaatt gtagctcaca ccaatgacca aattaaaata 540
ataaaagcgt gcgcatatatt catgtacaac tttctaactc tccacccttt caatgatggg 600

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aatggaagaa cagctagatt attgtatagt tttctattga aaggtaatgg tatcgtacct 660
 catttttcac ccataacaca ccctagggat caatttgttg atacttttagt gtatttttaga 720
 gaacatggag atggacgacc tttattgtat gttttgctgg aatcaataaa aaataagtaa 780

<210> 73
 <211> 255
 <212> PRT
 <213> SHRIMP

<400> 73
 Met Ser Thr Cys Ser Asn Leu Leu Ser Val Phe Gly Gly Gly Asp Trp
 1 5 10 15
 Thr Thr Thr Phe Pro Phe Asp Leu Val His Thr Arg Gln Glu Cys Asp
 20 25 30
 Lys Lys Arg Glu Gln Asp Tyr Ser Phe Phe Ile Thr Glu Thr Cys Lys
 35 40 45
 Gly Glu Asn Ile Gly Ile His Ser Tyr Glu His Thr Ser Lys Ile Ile
 50 55 60
 Asp Thr Gly Asn Asn Asp Ser Thr Ser Ile Glu Glu Leu Glu Val Leu
 65 70 75 80
 Asn Ile Tyr Lys Ala Ile Asn His Leu Glu Asn Ile Leu Lys Leu Asn
 85 90 95
 Lys Gly Glu Lys Ile Ile Leu Met Asp Val Glu Thr Met Ile Thr His
 100 105 110
 Lys Ile Leu Met Lys Gly Ile Leu Pro Lys Gly Lys Asn Gly Ser Phe
 115 120 125
 Ser Thr Cys Val Arg Phe Ala Val Asn Lys Asn Asn Glu Arg His Tyr
 130 135 140
 Tyr Pro Val Phe Glu Thr Glu Lys Glu Ala Phe Asn Ser Ile Gln Asn
 145 150 155 160
 Leu Val Asp Tyr Tyr Asn Glu Ile Val Ala His Thr Asn Asp Gln Ile
 165 170 175
 Lys Ile Ile Lys Ala Cys Ala Tyr Phe Met Tyr Asn Phe Leu Thr Leu
 180 185 190
 His Pro Phe Asn Asp Gly Asn Gly Arg Thr Ala Arg Leu Lys Phe Leu
 195 200 205
 Leu Lys Gly Asn Gly Ile Val Pro His Phe Ser Pro Ile Thr His Pro
 210 215 220
 Arg Asp Gln Phe Val Asp Thr Leu Val Tyr Phe Arg Glu His Gly Asp
 225 230 235 240
 Gly Arg Pro Leu Leu Tyr Val Leu Leu Glu Ser Ile Lys Asn Lys
 245 250 255

<210> 74
 <211> 480
 <212> DNA
 <213> SHRIMP

<400> 74
 atggaggacc taaaatccac tatcgagaga gtatatgaag aaagagtgga gaatctagaa 60
 caatggacaa atactgtaga ggaagaagaa aggactgtct cagcaatcga ttctgtcctg 120
 gaggaacaaa aaagggccct ggacgcatgg gaagcagcga taaaggaacg agaaaacgac 180
 ctgcagtaa aagaagggat atctgcactc gttttcaacg cagcagacgc caaaacacgt 240
 aaagaattga taaatacgtg gatagccgaa agggaaacgt cagaaaaaag aagaaaggaa 300
 gcaacctcta ccaataatca actgaagaac cagatgtcat ctctagtcaa cacaaccaa 360
 acactcaaag aaaagtacaa caaatattac agaagaagtg ccataactcaa catgcaatac 420
 atcaataaca aaagggatta tgaagcaagt caattttggg tgtatacaaa caatgcataa 480

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165

<210> 75
 <211> 159
 <212> PRT
 <213> SHRIMP

<400> 75

Met	Glu	Asp	Leu	Lys	Ser	Thr	Ile	Glu	Arg	Val	Tyr	Glu	Glu	Arg	Val
1				5					10					15	
Glu	Asn	Leu	Glu	Gln	Trp	Thr	Asn	Thr	Val	Glu	Glu	Glu	Glu	Arg	Thr
		20					25						30		
Val	Ser	Ala	Ile	Asp	Ser	Val	Leu	Glu	Glu	Gln	Lys	Arg	Ala	Leu	Asp
		35					40					45			
Ala	Trp	Glu	Ala	Ala	Ile	Lys	Glu	Arg	Glu	Asn	Asp	Leu	Ala	Val	Lys
	50					55				60					
Glu	Gly	Ile	Ser	Ala	Leu	Val	Phe	Asn	Ala	Ala	Asp	Ala	Lys	Thr	Arg
65					70				75					80	
Lys	Glu	Leu	Ile	Asn	Thr	Trp	Ile	Ala	Glu	Arg	Glu	Thr	Ser	Glu	Lys
				85					90					95	
Arg	Arg	Lys	Glu	Ala	Thr	Ser	Thr	Asn	Asn	Gln	Leu	Lys	Asn	Gln	Met
			100					105					110		
Ser	Ser	Leu	Val	Asn	Thr	Thr	Lys	Thr	Leu	Lys	Glu	Lys	Tyr	Asn	Lys
		115					120					125			
Tyr	Tyr	Arg	Arg	Ser	Ala	Ile	Leu	Asn	Met	Gln	Tyr	Ile	Asn	Asn	Lys
	130					135					140				
Arg	Asp	Tyr	Glu	Ala	Ser	Gln	Phe	Trp	Val	Tyr	Thr	Asn	Asn	Ala	
145					150					155					

<210> 76
 <211> 321
 <212> DNA
 <213> SHRIMP

<400> 76

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ggtggcggcg	gaaacgagga	acagaagagc	ggacccagcc	agaagcatca	tatccctggg	180
cctgttctta	tatttgtcct	catcatcggt	atcggtggca	gtgtcgatcat	catcatcggt	240
gtccttatca	gtgtcaggat	cgctgtcctt	ctttggtccc	atccatacat	tcatgacggc	300
caggacgagg	ataccaattg	a				321

<210> 77
 <211> 106
 <212> PRT
 <213> SHRIMP

<400> 77

Met	His	Lys	Phe	Ser	Asn	Lys	Phe	Tyr	Phe	Ile	Ile	Lys	Gly	Val	Leu
1				5					10					15	
Ile	Ile	Ile	Phe	Val	Pro	Asp	Val	Val	Phe	Ser	Ile	Phe	Leu	Leu	Pro
			20					25					30		
Pro	Leu	Gly	Val	Arg	His	Lys	Asn	Gly	Gly	Gly	Gly	Asn	Glu	Glu	Gln
		35					40					45			
Lys	Ser	Gly	Pro	Ser	Gln	Lys	His	His	Ile	Pro	Gly	Pro	Val	Leu	Ile
	50					55				60					
Phe	Val	Leu	Ile	Ile	Val	Ile	Val	Gly	Ser	Val	Val	Ile	Ile	Ile	Gly
65					70				75					80	
Val	Leu	Ile	Ser	Val	Arg	Ile	Ala	Val	Leu	Leu	Trp	Ser	His	Pro	Tyr
				85				90						95	
Ile	His	Asp	Gly	Gln	Asp	Glu	Asp	Thr	Asn						
			100					105							

<210> 78
 <211> 1635
 <212> DNA
 <213> SHRIMP

<400> 78
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 ggagaaccac cttctcataa aatgagggga cttctttata gcgttttagg acctgatccg 180
 tgcgaggacc cagaaagggg atatatgtgat attgtagtgt ctattttgca gacaaataat 240
 atacaggtaa caaaagaatg ggaattgttt tccgataagt tgagaaaatt ggggtccatgg 300
 attgatagga gcggaattga gaataatggc gaaggagaag aagatggaga tgaaaatgaa 360
 gacgggggtg gaaatggggg aagaattgaa gacagagaag cacatcgacg aaaaatgatg 420
 aagaaattgt cttttgttgg aagagaagat ccagtcgctg tagatttacc cacgtggcga 480
 gaaaacagta cagaatttgc acgtcgttta acactcaagg aattgtgcga tttaatagtt 540
 gaatgtggat gcacaaaatc aaaagaggaa ctctttgact tcatttttga agaaccgtgg 600
 gagattaaag aggctgctga cgtaggggtg atggcaaaca ggagtaaatt caccaaggaa 660
 tcattaattg actggttttt tgagttcgac acatatagta aatgtgtagt attttttgaa 720
 gcagtcaact ggtacttgaa atctcaagcg tctccaattt cattggtact agatgatata 780
 tattgttgtg tcttttccta cataagacgc caaacctttt taactagggc aaaaaaccca 840
 tctttaacag tggcttcac cttttctccc acgcccga caaagctttt ggctatcgac 900
 gagtgcgtgc aacacttttt aaaatcagac attaatatta gccagatggc attaactgaa 960
 agggactgct tcttcctctt ttttaactgaa atgccccgcc aacaaaaaaa agtaaacacc 1020
 ttccctggaca caatgaagag acctacctta tctcttctac cttccacctc ctctcctct 1080
 tcttccaaca acaagagaaa gagaaatact gccgctgcc aatattcttct tccagtgtac 1140
 aggagtaact tttctacagc atccaataac aagagactga aaactgatga tggggaaaat 1200
 gcatcagcct gtattcttat cgaaggggat gcgaatggaa aaataagccc tataaggatt 1260
 atggtaagaa aatcaactat tattccagaa gtgtttaacc atcttttgtt ccctgtcttt 1320
 gcctctaaag acactggtgc gaatatctta ttttttatca aaatgaaatc ctttgcaagt 1380
 gcactcttac tctccctgg actttttaga caccctaaac aatttctcaa cgggccgtgc 1440
 aaatggatga ctctagcaga aaacaacatc aacgacaaca acataaactc ttccacgatg 1500
 tggagttaca cgctagcaga ttattgtcct ctgggctatt acaccaaga gagccctcaa 1560
 ccctatcaga catgcggcaa ttttacttcg actacaaaca agagactaca aaacgtgcag 1620
 ccattatact ttttaa 1635

<210> 79
 <211> 540
 <212> PRT
 <213> SHRIMP

<400> 79
 Met Phe Arg Gln Phe Cys Ser Leu Tyr Leu Leu Gln Arg Arg Val Asn
 1 5 10 15
 Asp Asn Leu Arg Ser Thr Ala Ser Ala Ser Ala Ala Ser Leu Lys
 20 25 30
 Gly Asp Gly Thr Glu Phe Ile Thr Gly Glu Pro Pro Ser His Lys Met
 35 40 45
 Arg Gly Pro Ser Tyr Ser Val Leu Gly Pro Asp Pro Cys Glu Asp Pro
 50 55 60
 Glu Arg Val Tyr Val Asp Ile Val Val Ser Ile Leu Gln Thr Asn Asn
 65 70 75 80
 Ile Gln Val Thr Lys Glu Trp Glu Leu Phe Ser Asp Lys Leu Arg Lys
 85 90 95
 Leu Gly Pro Trp Ile Asp Arg Ser Gly Ile Glu Asn Asn Gly Glu Gly
 100 105 110
 Glu Glu Asp Gly Asp Glu Asn Glu Asp Gly Gly Gly Asn Gly Gly Arg
 115 120 125
 Ile Glu Asp Arg Glu Ala His Arg Arg Lys Met Met Lys Lys Leu Ser
 130 135 140

Phe	Val	Gly	Arg	Glu	Asp	Pro	Val	Ala	Val	Asp	Leu	Pro	Thr	Trp	Arg
145					150					155					160
Glu	Asn	Ser	Thr	Glu	Phe	Ala	Arg	Arg	Leu	Thr	Leu	Lys	Glu	Leu	Cys
				165					170						175
Asp	Leu	Ile	Val	Glu	Cys	Gly	Cys	Ile	Lys	Ser	Lys	Glu	Glu	Leu	Phe
			180					185					190		
Asp	Phe	Ile	Phe	Glu	Glu	Pro	Trp	Glu	Ile	Lys	Glu	Ala	Ala	Asp	Val
		195					200					205			
Arg	Gly	Met	Ala	Asn	Arg	Ser	Lys	Phe	Thr	Lys	Glu	Ser	Leu	Ile	Asp
	210					215					220				
Trp	Phe	Phe	Glu	Phe	Asp	Thr	Tyr	Ser	Lys	Cys	Val	Val	Phe	Phe	Glu
225					230					235					240
Ala	Val	Asn	Trp	Tyr	Leu	Lys	Ser	Gln	Asp	Ile	Ser	Leu	Val	Leu	Asp
				245					250					255	
Asp	Ile	Tyr	Cys	Cys	Val	Phe	Ser	Tyr	Ile	Arg	Arg	Gln	Thr	Phe	Leu
			260					265					270		
Thr	Arg	Ala	Lys	Asn	Pro	Ser	Leu	Thr	Val	Ala	Ser	Ser	Phe	Ser	Pro
		275					280					285			
Thr	Pro	Asp	Thr	Lys	Leu	Leu	Ala	Ile	Asp	Glu	Cys	Val	Gln	His	Phe
	290					295					300				
Leu	Lys	Ser	Asp	Ile	Asn	Ile	Ser	Gln	Met	Ala	Leu	Thr	Glu	Arg	Asp
305					310					315					320
Cys	Phe	Phe	Pro	Leu	Leu	Thr	Glu	Met	Pro	Arg	Gln	Gln	Lys	Lys	Val
				325					330					335	
Asn	Thr	Phe	Leu	Asp	Thr	Met	Lys	Arg	Pro	Thr	Leu	Ser	Leu	Leu	Pro
			340					345					350		
Ser	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Asn	Asn	Lys	Arg	Lys	Arg	Asn	Thr
		355					360					365			
Ala	Ala	Ala	Asn	Ile	Leu	Leu	Pro	Val	Tyr	Arg	Ser	Asn	Phe	Ser	Thr
	370					375					380				
Asn	Asn	Lys	Arg	Leu	Lys	Thr	Asp	Asp	Gly	Glu	Asn	Ala	Ser	Ala	Cys
385					390					395					400
Ile	Leu	Ile	Glu	Gly	Tyr	Ala	Asn	Gly	Lys	Ile	Ser	Pro	Ile	Arg	Ile
				405					410					415	
Met	Val	Arg	Lys	Ser	Thr	Ile	Ile	Pro	Glu	Val	Phe	Asn	His	Leu	Leu
			420					425					430		
Phe	Pro	Val	Phe	Ala	Ser	Lys	Asp	Thr	Gly	Ala	Asn	Ile	Leu	Phe	Phe
		435					440					445			
Ile	Lys	Met	Lys	Ser	Phe	Ala	Ser	Ala	Ser	Leu	Leu	Leu	Pro	Gly	Leu
		450				455					460				
Phe	Arg	His	Pro	Lys	Gln	Phe	Leu	Asn	Gly	Pro	Cys	Lys	Trp	Met	Thr
465					470					475					480
Leu	Ala	Glu	Asn	Asn	Ile	Asn	Asp	Asn	Asn	Ile	Asn	Ser	Ser	Thr	Met
				485					490					495	
Trp	Ser	Tyr	Thr	Leu	Ala	Asp	Tyr	Cys	Pro	Leu	Gly	Tyr	Tyr	Thr	Gln
			500					505					510		
Glu	Ser	Pro	Gln	Pro	Tyr	Gln	Thr	Cys	Gly	Asn	Phe	Thr	Ser	Thr	Thr
		515					520					525			
Asn	Lys	Arg	Leu	Gln	Asn	Val	Gln	Pro	Leu	Tyr	Phe				
	530					535					540				

<210> 80

<211> 582

<212> DNA

<213> SHRIMP

<400> 80

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gagttacacg cttagcagatt attgtcctct gggctattac acccaagaga gccctcaacc 120
ctatcagaca tgcggcaatt ttacttcgac taaaacaag agactacaaa acgtgcagcc 180

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attatacttt taaacactct tttggaatac tacaggacac cttcagaaga gtgggaaatt 240
ccgtttaatc tcttgcttaa tgtgatgaat aacaagtgga gtacactcat tccagggtgc 300
aaaataagtg caggatcat atcgaaactc ccatggacca tgaaaacaat gtacgagatt 360
gtttcttcgc ccaataataa taataacaac ggagactact attctacatg caggcgaatg 420
gtaatggaat atcctatcgg ggggtttattg cacacgcctg ccataactaa taagtatcca 480
cgctccagaa tggtcacctg tacaaagggc aaagaccacc agaagctata tgacatctct 540
agacaaatgt ttgatataat agaagcaaat ggacaactct ga 582

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<210> 81
 <211> 193
 <212> PRT
 <213> SHRIMP

<400> 81
 Met Asp Asp Ser Ser Arg Lys Gln His Gln Arg Gln Gln His Lys Leu
 1 5 10 15
 Phe His Asp Val Glu Leu His Ala Ser Arg Leu Leu Ser Ser Gly Leu
 20 25 30
 Leu His Pro Arg Glu Pro Ser Thr Leu Ser Asp Met Arg Gln Phe Tyr
 35 40 45
 Phe Asp Tyr Lys Gln Glu Thr Thr Lys Arg Ala Ala Ile Ile Leu Leu
 50 55 60
 Asn Thr Leu Leu Glu Tyr Tyr Arg Thr Pro Ser Glu Glu Trp Glu Ile
 65 70 75 80
 Pro Phe Asn Leu Leu Asn Val Met Asn Asn Lys Trp Ser Thr Leu
 85 90 95
 Ile Pro Gly Val Lys Ile Ser Ala Gly Ile Ile Ser Lys Leu Pro Trp
 100 105 110
 Thr Met Lys Thr Met Tyr Glu Ile Val Ser Ser Pro Asn Asn Asn Asn
 115 120 125
 Asn Asn Gly Asp Tyr Tyr Ser Thr Cys Arg Arg Met Val Met Glu Tyr
 130 135 140
 Pro Ile Gly Gly Leu Leu His Thr Pro Ala Ile Thr Asn Lys Tyr Pro
 145 150 155 160
 Arg Ser Arg Met Val Thr Cys Thr Lys Gly Lys Asp His Gln Lys Leu
 165 170 175
 Tyr Asp Ile Ser Arg Gln Met Phe Asp Ile Ile Glu Ala Asn Gly Gln
 180 185 190
 Leu

<210> 82
 <211> 615
 <212> DNA
 <213> SHRIMP

<400> 82
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 acagacaata tcgagacaaa catggatgaa aacctccgca ttctgtgac tgctgagggt 180
 ggatcaggct acttcaagat gactgatgtg tcttttgaca gcgacacctt gggcaaaatc 240
 aagatccgca atggaaagtc tgatgcacag atgaaggaa aagatgcgga tcttgtcatc 300
 actcccgtgg agggccgagc actcgaagtg actgtggggc agaatctcac ctttgaggga 360
 acattcaagg tgtggaacaa cacatcaaga aagatcaaca tcaactggtat gcagatggtg 420
 ccaaagatta acccatcaaa ggcctttgtc ggtagctcca acacctctc cttcaccocc 480
 gtctctattg atgaggatga agttggcacc tttgtgtgtg gtaccacctt tggcgaccca 540
 attgcagcta ccgccgtgg aaatcttttc gacatgtacg tgcacgtcac ctactctggc 600
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<210> 83

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<211> 204
 <212> PRT
 <213> SHRIMP

<400> 83

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Met Asp Leu Ser Phe Thr Leu Ser Val Val Ser Ala Ile Leu Ala Ile
 1          5          10          15
Thr Ala Val Ile Ala Val Phe Ile Val Ile Phe Arg Tyr His Asn Thr
          20          25          30
Val Thr Lys Thr Ile Glu Thr His Thr Asp Asn Ile Glu Thr Asn Met
          35          40          45
Asp Glu Asn Leu Arg Ile Pro Val Thr Ala Glu Val Gly Ser Gly Tyr
          50          55          60
Phe Lys Met Thr Asp Val Ser Phe Asp Ser Asp Thr Leu Gly Lys Ile
65          70          75          80
Lys Ile Arg Asn Gly Lys Ser Asp Ala Gln Met Lys Glu Glu Asp Ala
          85          90          95
Asp Leu Val Ile Thr Pro Val Glu Gly Arg Ala Leu Glu Val Thr Val
          100          105          110
Gly Gln Asn Leu Thr Phe Glu Gly Thr Phe Lys Val Trp Asn Asn Thr
          115          120          125
Ser Arg Lys Ile Asn Ile Thr Gly Met Gln Met Val Pro Lys Ile Asn
130          135          140
Pro Ser Lys Ala Phe Val Gly Ser Ser Asn Thr Ser Ser Phe Thr Pro
145          150          155          160
Val Ser Ile Asp Glu Asp Glu Val Gly Thr Phe Val Cys Gly Thr Thr
          165          170          175
Phe Gly Ala Pro Ile Ala Ala Thr Ala Gly Gly Asn Leu Phe Asp Met
          180          185          190
Tyr Val His Val Thr Tyr Ser Gly Thr Glu Thr Glu
          195          200

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<210> 84
 <211> 888
 <212> DNA
 <213> SHRIMP

<400> 84

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ttttattttt ctggtgccat aattgaatgt aaaaaaataa ggataataat gatgttcctt 120
ttattatctc tcatactttt tgtgtgtttt gtgggtgtgg tggtttgtgt gattttcatg 180
tcacgaccaa ataaaactac tacaacatcc aataaaaaaa caaagaaaga taaagagaag 240
gaaaaagaag atgacaccga aggagctgta ttagggcgaa gggaacctga aaataggccg 300
atcggaagag acgaggaagg tgctgtagaa gacggaaaag aagaggagga agtttttgaa 360
tttgaacaac cgagtgtaaa tactgggtcc aatacaggag gtggaggaac aggaactgtg 420
cctggagaag gtttgttacc tccaccccct cctactccta ctccactacc tccacctact 480
cctactccta ctccctccacc tcccccgaca cgaaccccat ctccctcttc atctcttggg 540
gaagatgatg atgatgatag agacatagac tttgatgata atgatataga cgaattttta 600
gatagtggag aagaaatgga agaagacgaa gaagaggaa atttgacac actcctttca 660
agactagaaa caggcatgag cggcgaagaa gtagattttg atgcatcatc tgcatatatt 720
caaccagatc ctgtagtgtt caaaaacata gaaaggtcag attatactct ggacccaatg 780
gagtcgtgga aagttttgaa cagatctgag ggagatatta gattcttcgt agatcgaggg 840
ataaccaaca agattaaagc catgacggaa gatctgaagg aactgtaa 888

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<210> 85
 <211> 295
 <212> PRT
 <213> SHRIMP

<400> 85

Met	Lys	Asn	Ser	Arg	Gln	Arg	Ser	Gly	Val	Trp	Arg	Gly	Asn	Ser	Cys
1				5					10				15		
Leu	Tyr	Lys	Ser	Phe	Tyr	Phe	Ser	Gly	Ala	Ile	Ile	Glu	Cys	Lys	Lys
			20					25				30			
Ile	Arg	Ile	Ile	Met	Met	Phe	Leu	Leu	Leu	Ser	Leu	Ile	Leu	Phe	Val
		35					40					45			
Cys	Phe	Val	Gly	Val	Val	Val	Gly	Val	Ile	Phe	Met	Ser	Arg	Pro	Asn
50						55				60					
Lys	Thr	Thr	Thr	Thr	Ser	Asn	Lys	Lys	Thr	Lys	Lys	Asp	Lys	Glu	Lys
65					70					75				80	
Glu	Lys	Glu	Asp	Asp	Thr	Glu	Gly	Ala	Val	Leu	Gly	Arg	Arg	Glu	Pro
				85				90						95	
Glu	Asn	Arg	Pro	Ile	Gly	Arg	Asp	Glu	Glu	Gly	Ala	Val	Glu	Asp	Gly
			100					105					110		
Lys	Glu	Glu	Glu	Glu	Val	Phe	Glu	Phe	Glu	Gln	Pro	Ser	Val	Asn	Thr
		115					120					125			
Gly	Ser	Asn	Thr	Gly	Gly	Gly	Gly	Thr	Gly	Thr	Val	Pro	Gly	Glu	Gly
130					135						140				
Leu	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Thr	Pro	Thr	Pro	Pro	Pro	Pro	Thr
145					150					155					160
Pro	Thr	Pro	Thr	Pro	Pro	Pro	Pro	Pro	Thr	Arg	Thr	Pro	Ser	Pro	Ser
				165					170					175	
Ser	Ser	Leu	Gly	Glu	Asp	Asp	Asp	Asp	Asp	Ile	Asp	Ile	Asp	Phe	Asp
			180					185					190		
Asp	Asn	Asp	Ile	Asp	Glu	Phe	Leu	Asp	Ser	Gly	Glu	Glu	Met	Glu	Glu
		195					200					205			
Asp	Glu	Glu	Glu	Glu	Asp	Leu	Asp	Thr	Leu	Leu	Ser	Arg	Leu	Glu	Thr
		210				215					220				
Gly	Met	Ser	Gly	Glu	Glu	Val	Asp	Phe	Asp	Ala	Ser	Ser	Ala	Tyr	Ile
225					230					235					240
Gln	Pro	Asp	Pro	Val	Val	Val	Lys	Asn	Ile	Glu	Arg	Ser	Asp	Tyr	Thr
				245					250					255	
Leu	Asp	Pro	Met	Glu	Ser	Trp	Lys	Val	Leu	Asn	Arg	Ser	Glu	Gly	Asp
			260					265						270	
Ile	Arg	Phe	Phe	Val	Asp	Arg	Gly	Ile	Thr	Asn	Lys	Ile	Lys	Ala	Met
		275					280						285		
Thr	Glu	Asp	Leu	Lys	Glu	Leu									
		290				295									

<210> 86

<211> 603

<212> DNA

<213> SHRIMP

<400> 86

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tctaaacaag aaaaatactc cacttctcat atcaatgaac aatttactgc caaacagttg 180
ccagtcactt acttgtcaaa aacgggtaaa ttaaaggaca tgcacttgac ccattccgat 240
tttatggcat atgttgatgt gcacaataga acaaaaactc tgaagcaccc catgtgtact 300
gacgaggctg gctgggcccc cttttgcctg ctggcttctg ctgaagctta tcgtcgcatc 360
cgttatggga gaggagaatt tggaccagaa aaacattccc tagctgaaac tatccaatcg 420
acagtacaag atatgtcgga gccatatata acccacatct tcaagaagaa cacggatggt 480
gatggacacg gaatgcaatc tgttttgag aagaatagga ataaaatcag aatgggtgat 540
ggaaaaacgt catcagaaac ttataatctt agtgataagt ctatatctat tgttggtgta 600
tag

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<210> 87

<211> 196

<212> PRT

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171

<213> SHRIMP

<400> 87

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Met Thr Met Trp Asn Lys Ile Val Ile Thr Thr Lys Arg Met Asn Trp
 1          5          10          15
Pro Met Val Val Gly Val Phe Phe Ile Leu Ala Ile Thr Ala Val Tyr
          20          25          30
Ile Arg His Ala Ser Lys Gln Glu Lys Tyr Ser Thr Ser His Ile Asn
          35          40          45
Glu Gln Phe Thr Ala Lys Gln Leu Pro Val Thr Tyr Leu Ser Lys Thr
          50          55          60
Gly Lys Leu Lys Asp Met His Leu Thr His Ser Asp Phe Met Ala Tyr
65          70          75          80
Val Asp Val His Asn Arg Thr Lys Thr Leu Lys His Pro Met Cys Thr
          85          90          95
Asp Glu Ala Gly Trp Ala His Phe Cys Leu Leu Ala Ser Ala Glu Ala
          100          105          110
Tyr Arg Arg Ile Arg Tyr Gly Arg Gly Glu Phe Gly Pro Glu Lys His
          115          120          125
Ser Leu Ala Glu Thr Ile Gln Ser Thr Val Gln Asp Met Ser Glu Pro
          130          135          140
Tyr Ile Thr His Ile Phe Lys Lys Asn Thr Asp Val Asp Gly His Gly
145          150          155          160
Met Gln Ser Val Leu Glu Lys Asn Arg Asn Lys Ile Arg Met Gly Asp
          165          170          175
Gly Lys Thr Ser Ser Glu Thr Tyr Asn Leu Ser Asp Lys Ser Ile Ser
          180          185          190
Ile Val Gly Val
          195

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<210> 88

<211> 861

<212> DNA

<213> SHRIMP

<400> 88

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gaaggggaag aacaggattt tgatgtatta gaactggact actccaaaat catccatgat 120
attactgcca tggtatctgt tgcagctcct cctcccaatt ccatactgga cgcactctgat 180
ggactaatag caactgcgtc tgcgacagca ccagcagccg aaacaggaaa ctctaacagg 240
atgaggctag ataaagacgt gtgccaacta atcgaaaggg acatagaatt agtgaagagt 300
gatactattg aagttgactc cattattcgc caactgttat attttgaga atctgcatca 360
gagaaaaaca taaaaaccaa ctctactgaa aaggagccag tttacttccc caaagaaccg 420
aaaggggagg cagtcaaact ggctaagaat accccagttc tagatacgat aacaaaacta 480
gattggatgg cgaacatctg ccaaagcaac aagatcgggg ttgaaaattt agcctctgcg 540
ttacaaagtg ggcaattaat atggacaact ttcccagctg ctgtatatgc ttcgttggaac 600
agcttttatc acattgctat aatgtggaaa cttttagggt cctttataaa catcgaagct 660
ttatcaaaag gatcaaagga caatcttttg cctcgtgatg atatacaggt tgtccatgct 720
aaacaggaga ttgctgcaat gcttcaatct agacaaaata ttctcggaag aggaccgctg 780
gaatatccgc ctgtgcctat cactgcaatt ctatcacgta ctataattcc cctgttgagg 840
aacttttctg agaaattatg a
          861

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<210> 89

<211> 286

<212> PRT

<213> SHRIMP

<400> 89

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Met Ser Ser Gly Ser Ile Asn Asn His Pro Ser Ser Asn Met Asp Thr
 1          5          10          15

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Asn	Lys	Met	Glu	Glu	Gly	Glu	Glu	Gln	Asp	Phe	Asp	Val	Leu	Glu	Leu
			20					25					30		
Asp	Tyr	Ser	Lys	Ile	Ile	His	Asp	Ile	Thr	Ala	Met	Leu	Ser	Val	Ala
		35					40					45			
Ala	Pro	Pro	Pro	Asn	Ser	Ile	Leu	Asp	Ala	Ser	Asp	Gly	Leu	Ile	Ala
	50					55					60				
Thr	Ala	Ser	Ala	Thr	Ala	Pro	Ala	Ala	Glu	Thr	Gly	Asn	Ser	Asn	Arg
65					70					75					80
Met	Arg	Leu	Asp	Lys	Asp	Val	Cys	Gln	Leu	Ile	Glu	Arg	Asp	Ile	Glu
				85				90						95	
Leu	Val	Lys	Ser	Asp	Thr	Ile	Glu	Val	Asp	Ser	Ile	Ile	Arg	Gln	Leu
			100					105					110		
Leu	Tyr	Phe	Gly	Glu	Ser	Ala	Ser	Glu	Lys	Asn	Ile	Lys	Thr	Asn	Ser
		115					120					125			
Thr	Glu	Lys	Glu	Pro	Val	Tyr	Phe	Pro	Lys	Glu	Pro	Lys	Gly	Glu	Ala
	130					135					140				
Val	Lys	Leu	Ala	Lys	Asn	Thr	Pro	Val	Leu	Asp	Thr	Ile	Thr	Lys	Leu
145					150					155					160
Asp	Trp	Met	Ala	Asn	Ile	Cys	Gln	Ser	Asn	Lys	Ile	Gly	Val	Glu	Asn
				165				170						175	
Leu	Ala	Ser	Ala	Leu	Gln	Ser	Gly	Gln	Leu	Ile	Trp	Thr	Thr	Phe	Pro
			180					185					190		
Ala	Ala	Val	Tyr	Ala	Ser	Leu	Asp	Ser	Phe	Tyr	His	Ile	Ala	Ile	Met
		195					200					205			
Trp	Lys	Leu	Leu	Gly	Ser	Phe	Ile	Asn	Ile	Glu	Ala	Leu	Ser	Lys	Gly
	210					215					220				
Ser	Lys	Asp	Asn	Leu	Leu	Pro	Arg	Asp	Asp	Ile	Gln	Val	Val	His	Ala
225					230				235						240
Lys	Gln	Glu	Ile	Ala	Ala	Met	Leu	Gln	Ser	Arg	Gln	Asn	Ile	Leu	Gly
				245					250					255	
Arg	Gly	Pro	Ser	Glu	Tyr	Pro	Pro	Val	Pro	Ile	Thr	Ala	Ile	Leu	Ser
			260					265					270		
Arg	Thr	Ile	Ile	Pro	Leu	Leu	Arg	Asn	Phe	Ser	Glu	Lys	Leu		
		275					280						285		

<210> 90
 <211> 696
 <212> DNA
 <213> SHRIMP

<400> 90
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 gtcgaggagg aacatgggca ggtaacaaca acaaacaaag aaatggcttc tactttctaca 180
 tcttcttcct catcctcctc ttctttctccc acgtcttcgg ccatcccttc aagcgatgag 240
 gaagaagaag aagaagaaga atatgactct gaatcagaca ctaacgtcga ttctcttctt 300
 ggagaggagg aggaagaaga ttcagataca gaatccacat ctgctgatgc aaactttcta 360
 cgatcttctt cacggaattc caccgaccaga aacaggctaa taaaaaagta cgttgataga 420
 tttatcaagt acgaaaagga tatttttactt gctgacagga ataaaaggaa gaagaggcac 480
 cgtaatcggc aaccccaaat acataagcta aacaacaaaa gactcaaaaa accaacagac 540
 aagaaacaga aaaccaataa gaagaaaact tggagaagac tccctaaatt tattaataaag 600
 atgtctcctg caagtagact gaaatttttc tctgcttgta taatatcagg gataaaaata 660
 acttctataa tagtactgtc gataatggcc ctttag 696

<210> 91
 <211> 231
 <212> PRT
 <213> SHRIMP

<400> 91

Met Asp Pro Gly Ala Ser Ala Ala Ser Arg Arg Ala Leu Trp Ser Ser
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 Thr Val Thr Asn Thr Arg His Tyr Gln Gln Gln Leu Asn Arg Ala Leu
 20 25 30
 Asn Lys Ile Glu Glu Glu Asp Asp Val Glu Glu Glu His Gly Gln Val
 35 40 45
 Thr Thr Thr Asn Lys Glu Met Ala Ser Thr Ser Thr Ser Ser Ser
 50 55 60
 Ser Ser Ser Ser Ser Pro Thr Ser Ser Ala Ile Pro Ser Ser Asp Glu
 65 70 75 80
 Glu Glu Glu Glu Glu Glu Glu Tyr Asp Ser Glu Ser Asp Thr Asn Val
 85 90 95
 Asp Ser Leu Leu Gly Glu Glu Glu Glu Asp Ser Asp Thr Glu Ser
 100 105 110
 Thr Ser Ala Asp Ala Asn Phe Leu Arg Ser Ser Ser Arg Asn Ser Thr
 115 120 125
 Thr Arg Asn Arg Leu Ile Lys Lys Tyr Val Asp Arg Phe Ile Lys Tyr
 130 135 140
 Glu Lys Asp Ile Leu Leu Ala Asp Arg Asn Lys Arg Lys Lys Arg His
 145 150 155 160
 Arg Asn Arg Gln Pro Gln Ile His Lys Leu Asn Asn Lys Arg Leu Lys
 165 170 175
 Lys Pro Thr Asp Lys Lys Gln Lys Thr Asn Lys Lys Lys Thr Trp Arg
 180 185 190
 Arg Leu Pro Lys Phe Ile Lys Lys Met Ser Pro Ala Ser Arg Leu Lys
 195 200 205
 Phe Phe Ser Ala Cys Ile Ile Ser Gly Ile Lys Ile Thr Ser Ile Ile
 210 215 220
 Val Leu Ser Ile Met Ala Leu
 225 230

<210> 92
 <211> 4608
 <212> DNA
 <213> SHRIMP

<400> 92
 atggctcaca aactttttatt tctggaggaa gaagatgcta aagagattgg caccctctcc 60
 caccagaac cttcattcgc tctttatgag agtgaaacat tccggtcggg gggcttctgc 120
 aaaaatgtaa ccgatgccta ccccaaattt cttcctcggc cgatggacat taattctgtg 180
 caggcactag cagtgcgtct agccctgatt caattctaca aaggagagg gtggaagaag 240
 aacatgtcca ttatagacct tgtgaaagat aagggtcgaaa ggaattttaa agtgacaag 300
 aaaacgagtg gaggatttat catcggagat ggtactgggt taggaaaaac aagagaattg 360
 gcagccttcg tcatgagtgt catactacaa gaaaaggcac tcttagatgt acaaaaacac 420
 gtagggccat caatttttgg tcaagattcg gacaaggtaa ttacggccat caacagtggc 480
 gtgtggaaaa ggcaccctt ttttatatgg ttgacgtgct ctaagcctct tttcaacagc 540
 tgtcaacagg gcatgcgaga agtggttaca aattctagag gtcttcgtga tcctaaattt 600
 tcatggagaa aactacaagt gccttgtgct aataaaccac cgtctttcaa gagcgacggg 660
 aaaagtgggt ccatgacagt agatgtggaa aattctgtat cgtctgctaa agactcgggtg 720
 gatattagat ttttactctt cagggtatgtt aaggaatttc atagtaagcg ttcttcaaga 780
 tcaataggag atttcttaac agaaacgccc accattttat ttatgacgta ctctgattta 840
 cgcacaaatc tggaaattgt actgaaattt ataacaggag gaacagacct cgattccaac 900
 aaggttatgc ccattgacaa ctttgtcaca gcattattat gtgacgagtt ccacaagact 960
 caaaatatta gtgactcttt tagaaaggaa ctggcaaaga cttgggagga agaagatact 1020
 agagttttgc gcaacatata aaaaagggca aacccttcag tgtcagacct tattaatagg 1080
 ttcaagagtg caatgagtga cgacagaaac tttaaagtga agcgcatgaa atcatccaat 1140
 aataagggcc gagttacaat gtccaactac ttgaaactat tatctcaagc tgatgcgttc 1200
 cgtattttct tagagatctt aaagtatgat acgttcacgg ttatggccag cgctacgcca 1260
 ttccagagca atgctgattt gcacatgatt gaccacatac taaggaaaag tgcgccagcc 1320
 tacacgagca tacaagcctt caaagaagtg tccagtgcata ctccagatgc tatggctgag 1380

cacagcgagt	acgtgacagt	gtttctggaa	caggttatta	aacttttaag	aaatagagga	1440
caattgggta	gtaggagtat	tagcatggct	ggagtcgact	gctctactac	taattgtaaa	1500
gcctccctc	ttcaaaaata	cgctatagac	gaattggctt	cgtactgttt	aaacgctaga	1560
caagtactca	tcgattctga	aaaagtagga	ggacatgtca	gaagggcctt	cacaaagatt	1620
atacgagaac	accaagaagg	aggaatattg	gaagaggaag	atggttgaaaa	attagtagca	1680
gagattaatt	ccccgtccag	aaagaggaaa	cgtgctgcaa	atgatgatga	tttatatgaa	1740
gtaattgaaa	atatcgacag	gcgttttaag	gtgggtggtg	tgcgcgatag	ggatgtcgca	1800
catgatggga	aaacaacact	aagaagtata	gtacaagatg	ctataaaaaac	ctactcacag	1860
aaaaaggatg	cgctttctaa	tggaggagga	ggaataataa	cgtctccgga	agttgacata	1920
agcagcattg	atatggttgc	tcaagattta	tacgatgcta	tcaagaaaaa	ggaaaaacct	1980
tccaaaggta	aaactgattt	taacgaagat	tatgacgacg	gtgctaataa	agaagacgga	2040
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<212> PRT

<213> SHRIMP

<400> 93

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<400> 95

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Gly	Cys	Ile	Phe	Ala	Leu	Val	Cys	Ala	Ala	Met	Ala	Tyr	Asn	Val	Ala	35	40	45	
Lys	Pro	Met	Ser	Val	Asn	Phe	Gln	Ala	Ile	His	Glu	Leu	Gly	Met	Lys	50	55	60	
Ser	Lys	Leu	Lys	Ala	Val	Gln	Gly	Ala	Asn	Pro	Glu	Lys	Thr	Leu	Glu	65	70	75	80
Glu	Tyr	Leu	Glu	Arg	Arg	His	Asp	Gly	Val	Glu	Asp	Asn	Tyr	Pro	Pro	85	90	95	
His	Pro	Ala	Leu	Leu	Asp	Met	Met	Asn	Leu	Thr	Val	Lys	Gly	Asn	Lys	100	105	110	
Trp	Asn	Val	Pro	Ser	Glu	Thr	Lys	Glu	Arg	Asn	Ser	Arg	Phe	Glu	Ser	115	120	125	
His	Asp	Leu	Ala	Ala	Asn	Arg	Ser	Ser	Ser	Leu	Leu	Val	Pro	Glu	His	130	135	140	
His	Ile	Asp	Arg	Leu	Ser	Glu	Ala	Thr	Ile	Glu	Lys	Ser	Asn	Lys	Tyr	145	150	155	160
Leu	Asp	Ala	Val	Ser	Gly	Lys	Lys	Phe	Arg	Gln	Arg	Met	Val	Asn	Leu	165	170	175	
Lys	Asp	Asn	Ile	Glu	Lys	Asp	Asp	Thr	Glu	Leu	Tyr	Asp	Ser	Leu	Phe	180	185	190	
Gly	Val	His	Asp	Ile	His	His	His	Ser	Ala	Ser	Gly	Val	Ser	Gly	Asp	195	200	205	
Ala	Pro	Pro	Pro	Pro	Pro	Ser	Thr	Ser	Glu	Gly	His	Asp	Glu	Asp	Val	210	215	220	
Asp	Ile	Leu	Ala	Tyr	Asn	Thr	Gly	Gly	Tyr	Cys	Ser	Asn	Pro	Val	Pro	225	230	235	240
Leu	Lys	Glu	Gly	Gln	Thr	Cys	Thr	Ser	Val	Cys	Tyr	Thr	Ser	Arg	Ala	245	250	255	
Val	Arg	Val	Met	Thr	Pro	Phe	Val	Ala	Gly	Gly	Thr	Phe	Ile	Thr	His	260	265	270	
Lys	Ser	Gly	Glu	Asp	Pro	Lys	Pro	Tyr	Cys	Trp	Ser	Gly	Asn	Val	Pro	275	280	285	
Gly	Asp	His	Ile	Glu	Thr	Ser	Pro	Thr	Thr	Gly	Glu	Arg	Val	Val	Lys	290	295	300	
Glu	Cys	Ser	Val	His	Thr	Ser	Ile	Val	Val	Leu	Thr	Asp	Asp	Gly	Gly	305	310	315	320
Trp	Gln	Cys	Arg	Pro	Lys	Tyr	Pro	Thr	Tyr	Phe	Gly	Gly	Ser	Gly	Gly	325	330	335	
Thr	Ser	Met	Thr	Ala	Cys	Ala	Phe	Asn	Pro	Ser	Thr	His	Lys	Gly	Pro	340	345	350	
Pro	Pro	Pro	Ser	Ser	Ser	Thr	Pro	Ile	Tyr	Tyr	Asp	Val	Leu	Lys	Lys	355	360	365	
Gln	Gln	Ile	Arg	Asn	His	Thr	Glu	Phe	Arg	Asn	Ser	Ser	Tyr	Ile	Ser	370	375	380	
Lys	Leu	Arg	Gln	Ser	Ser	Ser	Leu	Ala	Glu	Phe	Lys	Ile	Lys	Cys	Asn				

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180

385					390					395					400
Asp	Pro	Glu	Phe	Leu	Tyr	Lys	Asn	Pro	Ile	Thr	Cys	Phe	Cys	Asn	Asn
				405					410					415	
Lys	Lys	Asp	Val	Leu	Asn	Asn	Asp	Leu	Leu	Ser	Gln	Asp	Val	Thr	Lys
			420					425					430		
Asp	Met	Lys	Phe	Arg	Gly	Met	Tyr	Glu	Cys	Met	Glu	Asn	Pro	Cys	Val
		435					440					445			
Met	Met	Pro	Asn	Ile	Asp	Pro	Ser	Phe	Val	Thr	Phe	Asp	Val	Ser	Thr
	450				455						460				
Met	Lys	Cys	Val	Pro	Gly	Val	Asn	Asn	Pro	Gln	Asp	Ser	Asn	Arg	His
465					470					475				480	
Ala	Ile	Ile	Gly	Asp	Asp	Arg	Thr	Pro	Leu	Val	Gly	Thr	Val	Pro	Ala
			485						490					495	
Met	Gly	Ile	Phe	Leu	Ala	Asp	Gln	Ser	Lys	Arg	Gly	Asp	Gln	Ile	His
		500					505						510		
Gln	Gln	Arg	Pro	Lys	Ser	Ser	Ile	Asp	Glu	Thr	Thr	Ala	Lys	Lys	Ile
	515						520					525			
Ala	Gln	Ala	Pro	Ile	Ile	Thr	Pro	Leu	Asn	Leu	Asp	Ala	Thr	Asn	Thr
	530					535					540				
Ser	Lys	Asn	Val	Leu	Phe	Val	Pro	Ile	Pro	Ser	Thr	Val	Leu	Pro	Pro
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Leu	Glu	Asn	Ile	Pro	His	Val	Ile	Ile	Arg	Pro	Ser	Ser	Leu	Leu	His
			565						570					575	
Arg	Ser	Cys	Leu	Ala	Pro	Val	Leu	Asn	Lys	Pro	Ser	Ser	Gly	Gln	His
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Arg	Pro	Phe	Cys	Thr	Ala	Pro	Phe	Tyr	Ile	Glu	Pro	Ala	Ala	Asn	Val
	595						600					605			
Leu	Ala	Gly	Asn	Ile	Pro	Gln	Lys	Pro	Tyr	Glu	His	Ser	Met	Leu	Ala
	610					615					620				
Thr	Glu	Cys	Leu	Arg	Asn	Ser	Arg	Met	Val	Ser	Gly	Ser	Val	His	Gly
625					630					635					640
Gly	Ser	Glu	Leu	Leu	Phe	Ser	Thr	Leu	Leu	Ser	Gln	Asn	Lys	Pro	Ser
			645						650					655	
Ser	Tyr	Ile	Arg	Thr	Pro	Pro	Gly	Gly	Thr	Pro	Ala	Pro	Glu	Tyr	Asn
		660					665					670			
Ser	Thr	Gly	Asp	Gln	Arg	Leu	Glu	Glu	Ile	Arg	Asp	Phe	Phe	Glu	Arg
		675					680					685			
Asn	Phe	Asn	Asp	Glu	Arg	Arg	Leu	Ser	Gln	Thr	Glu	Tyr	Val	Ile	Lys
	690					695					700				
Lys	His	Arg	Met	Arg	Thr	Ser	Glu	Ile	Tyr	Leu	Lys	Ser	Ser	Ser	Trp
705					710					715					720
Asp	Ser	Leu	Met	Lys	Arg	Lys	Glu	Phe	Leu	Arg	His	Ile	Ile	Lys	Lys
			725						730					735	
Ser	Glu	Asp	Thr	Phe	Val	Leu	Lys	Glu	Gly	Leu	Leu	Met	Arg	Ser	Tyr
		740						745				750			
Gly	Pro	Tyr	Ala	Ala	Thr	Val	Leu	Ala	Arg	Asp	Met	Phe	Asp	Leu	Asp
	755						760					765			
Tyr	Leu	Lys	Gly	Lys	Pro	Ala	Ser	Lys	Thr	Ser	Ser	Thr	Leu	Lys	Val
	770					775						780			
Ser	Asn	Pro	Leu	Gln	Tyr	Ala	Phe	Pro	Thr	Ser	Tyr	Ser	Val	Leu	Pro
785					790					795				800	
Glu	Glu	Gly	Ala	Thr	Asp	Asp	Ile	Phe	Ser	Val	Asp	His	Asn	Arg	Ile
			805						810					815	
Phe	Asp	Ser	Glu	Thr	Ile	Pro	Ser	Tyr	Phe	Asp	Cys	Ser	Asn	Val	Thr
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Pro	Gly	Ser	Glu	Lys	Leu	Phe	Gly	Thr	Ser	Ser	Ser	Ser	Ser	Glu	Tyr
	835						840					845			
Arg	Val	Asp	Ile	Asp	Asp	Asp	Ala	Trp	Gly	Leu	Gln	Ser	Phe	Arg	Leu
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Asp	His	Asn	Pro	Lys	Ser	Gly	Pro	Val	Val	Gln	Ser	Asp	Pro	Arg	Leu
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			20					25					30		
Pro	Asn	Ser	Gly	Lys	Glu	Ile	Met	Glu	Asn	Arg	Leu	Ile	His	Lys	Gly
		35					40					45			
Lys	Cys	Gly	Ala	Phe	Glu	Ala	Asp	Thr	Gln	Leu	Ala	Tyr	Phe	Phe	Pro
	50					55					60				
Ser	Asn	Asn	Glu	Glu	Asn	Thr	Lys	Lys	Leu	Asn	Ile	Gly	Phe	Gln	Ile
65					70					75					80
Lys	Ser	Asn	Cys	Leu	Ser	Phe	Phe	Ile	Arg	Asp	Phe	Leu	Asn	Asp	Trp
				85					90					95	
Leu	Glu	Glu	Ile	Lys	Asp	Cys	Gly	Pro	Tyr	Cys	Thr	Phe	Ser	Gln	Tyr
			100					105					110		
Met	Asp	Gly	Asp	Lys	Glu	Ile	Phe	Gly	Asn	Ser	Val	Phe	Gly	Gln	Asp
		115					120					125			
Phe	Thr	Ile	Val	Ala	Met	Asp	Trp	Ile	Asp	Lys	Gly	Val	Thr	Phe	Tyr
	130					135					140				
Ile	Phe	Val	Asp	Gly	Ser	Asp	Ser	Met	Glu	Asn	Met	Ala	Ser	Leu	Trp
145					150					155				160	
Met	Cys	Asp	Lys	Leu	Lys	Arg	Met	Asn	Ala	Asn	Val	Val	Lys	Val	Phe
				165					170					175	

Val	Asp	Asn	Ala	Ser	Lys	Pro	Lys	Phe	Ser	Val	Cys	Lys	Thr	Cys	Arg
			180					185					190		
Trp	Glu	Phe	Pro	Gly	Pro	Val	Ser	Tyr	Val	Ile	Glu	Gly	His	Gly	Met
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Gly	His	Ser	Asp	Leu	Ser	Cys	Asp	Glu	Ile	Ser	Glu	Phe	Leu	Val	Gln
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 <212> DNA
 <213> SHRIMP

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 ttgatgttca atgataaccgc attaacacag tttgcccaga gaggatacga gcctagttata 180
 cccaccatat tgaaagctgc ttttagatttc tctctccaag aagaagaacc ccttggttgct 240
 gccaccggtc tcgatgtcaa taaagcacct cgttcttggc caatactgaa ttgtcgcttg 300
 gggatatattg catcctcaaa ttatccttgg gctgaacaca taatttctgg ggataaggaa 360
 gaaattaaaaa gggctctaga agaacatgag aagaatgcta atgtgcgttt cgacagcgat 420
 aattgtccag tgtgtttaga agatttcagt agtaccaata tcatcaggac gacacgctgt 480
 ggacattgta ttgatgaaaa atgttgggac agattggtgt tgagtacgca acgtggagaa 540
 attaccgggt gtcctgtatg cagagaacgt acttccttaa gacctgacgc tgatcaagtt 600
 aaagagatgt tggttgaacc aatagtgtct tgtaaaagaa tggcagtgcc tgatgaacaa 660
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 tggacagatg agtccgaaac tgtatga 747

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 <211> 248
 <212> PRT
 <213> SHRIMP

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 Leu Ser Val Thr Glu Ala Ala Leu Leu Met Phe Asn Asp Thr Ala Leu
 35 40 45
 Thr Gln Phe Ala Gln Arg Gly Tyr Glu Pro Ser Ile Pro Thr Ile Leu
 50 55 60
 Lys Ala Ala Leu Asp Phe Ser Leu Gln Glu Glu Pro Leu Val Ala
 65 70 75 80
 Ala Thr Gly Leu Asp Val Asn Lys Ala Pro Arg Ser Trp Pro Ile Leu
 85 90 95
 Asn Cys Arg Leu Gly Tyr Ile Ala Ser Ser Asn Tyr Pro Trp Ala Glu
 100 105 110
 His Ile Ile Ser Gly Asp Lys Glu Ile Lys Arg Ala Leu Glu Glu
 115 120 125
 His Glu Lys Asn Ala Asn Val Arg Phe Asp Ser Asp Asn Cys Pro Val
 130 135 140
 Cys Leu Glu Asp Phe Ser Ser Thr Asn Ile Ile Arg Thr Thr Arg Cys
 145 150 155 160
 Gly His Cys Ile Asp Glu Lys Cys Trp Asp Arg Leu Val Leu Ser Thr
 165 170 175
 Gln Arg Gly Glu Ile Thr Arg Cys Pro Val Cys Arg Glu Arg Thr Ser
 180 185 190
 Leu Arg Pro Asp Ala Asp Gln Val Lys Glu Met Leu Val Glu Pro Ile
 195 200 205
 Val Ser Cys Lys Arg Met Ala Val Pro Asp Glu Gln Val Ser Cys Lys

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183

210 215 220
 Arg Arg Arg Ile Gly Tyr Asn Arg Tyr Gln Phe Leu Ile Asn Asp Val
 225 230 235 240
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 attacctcca gaaattctcc tcctgttccct tcaagtagtt tcaagaaatt agacaataaa 180
 gaagagtttta gagatattat ctacttcttt atcaacaaca ataccaagtc tgattcttcc 240
 cccactctgcg agggaaatgac ttttatcaac gcattgacaa ccgtctgcaa aaccttcaga 300
 ggccttttacg aaaacatcca cgacgacttt ttgttcgtaa aatattctct tctggtctct 360
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 tgcaattttc ttgatgctct tgctaaaaaa tacaagaata taatatacga tttcgataga 1740
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 <212> PRT
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 Glu Leu Ala Leu Leu Asn Asp Ile Ile Thr Ser Arg Asn Ser Pro Pro
 35 40 45
 Val Pro Ser Ser Ser Phe Lys Lys Leu Asp Asn Lys Glu Glu Phe Arg
 50 55 60
 Asp Ile Ile Tyr Phe Phe Ile Asn Asn Asn Thr Lys Ser Asp Ser Ser
 65 70 75 80
 Pro Ile Cys Glu Gly Met Thr Phe Ile Asn Ala Leu Thr Thr Val Cys

				85					90					95	
Lys	Thr	Phe	Arg	Gly	Glu	Asn	Ile	His	Asp	Asp	Phe	Leu	Phe	Val	Lys
			100					105					110		
Tyr	Ser	Leu	Leu	Val	Ser	Met	Asp	Asn	Gly	Phe	Leu	Arg	Arg	Glu	Thr
		115					120					125			
His	Gly	Ile	Lys	Phe	Gly	Thr	Gly	Asp	Asp	Ser	Arg	Thr	Gly	Phe	Lys
		130				135					140				
Phe	Thr	Ser	Lys	Glu	Gln	Ala	Glu	Glu	Glu	Arg	Glu	Lys	Val	Met	Arg
145				150						155				160	
Arg	Ile	Lys	Lys	Leu	Asp	Gly	Val	Leu	Ala	Ser	Leu	Lys	Lys	Ser	Thr
				165					170					175	
Ser	Ser	Ala	Arg	Ser	Gly	Ile	Val	Phe	Tyr	Val	Glu	Lys	Cys	Ser	Ser
			180					185					190		
Val	Ile	Arg	Phe	Arg	Leu	Phe	Ser	Arg	Ile	Val	Asn	Ile	Thr	Ser	Asp
		195					200				205				
Tyr	Val	Ala	Glu	Met	Lys	Lys	Ser	Ala	Pro	Leu	Glu	Pro	Phe	Asp	Ile
		210				215					220				
Ser	Phe	Gly	Tyr	Lys	Tyr	Phe	Val	Asp	Glu	Ser	Pro	Cys	Val	Thr	Lys
225				230					235					240	
Ala	Lys	Arg	Leu	Ile	Ser	Asn	Gly	Asn	Phe	Ile	Ile	Gly	Arg	Pro	Phe
				245				250					255		
Ser	Cys	Leu	Glu	Thr	Ser	Pro	Ser	Ser	Val	Ser	Thr	Asp	Phe	Arg	Glu
			260					265					270		
Glu	Met	Asn	Met	Asp	Ala	Arg	Ser	Ile	Ala	Arg	Leu	Asn	Trp	Thr	Asn
		275					280					285			
Glu	Glu	Arg	Ala	Ser	Ala	Tyr	Arg	Ser	Val	Ile	Ile	Lys	Ser	Phe	Leu
		290				295				300					
Ser	Ser	Ile	Glu	Glu	Glu	Met	Val	Glu	Glu	Tyr	Cys	Glu	Thr	Thr	Thr
305				310						315				320	
Lys	Thr	Val	Ala	Glu	Met	Ala	Val	Glu	Phe	Val	Asp	Val	Phe	Ile	Glu
				325				330					335		
Lys	Ala	Glu	Thr	Ile	Gln	His	Phe	Gln	Thr	Lys	Ile	Phe	Asp	Thr	Met
			340				345					350			
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		355					360					365			
Ile	Asn	Glu	Ala	Val	Gly	Ser	Gly	Leu	Cys	Gly	Ala	Ile	Leu	Leu	Trp
		370				375				380					
Met	Ile	Asn	Ser	Arg	Pro	Phe	Glu	Glu	Ile	Asp	Tyr	Asn	Tyr	Phe	Lys
385				390						395				400	
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				405					410				415		
Asp	Asn	Leu	Ile	Val	Lys	Arg	Ile	Val	Ser	His	Lys	Asn	Val	Val	Ile
			420					425				430			
Thr	Asp	Phe	Val	Lys	Gly	Tyr	Val	Arg	Leu	Cys	Val	Lys	Val	Ser	Cys
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<211> 1197
<212> DNA
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gaaaatgatg ctctgagagc atctatagaa agtacctgct cagcactcaa taggtttcct 300
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gatagggtca gagacggcag acgcaacact tcacggagga catctgccgt catggccagg 1140
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<211> 396
<212> PRT
<213> SHRIMP

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35 40 45
Glu Met Met Lys Lys His Lys Lys Arg Met Glu Ile Lys Asp Met Val
50 55 60
Lys Lys Cys Ala Ser Cys Lys Lys Val Asp Tyr Ser Ser Ser Thr Leu
65 70 75 80
Glu Asn Asp Ala Leu Arg Ala Ser Ile Glu Ser Thr Cys Ser Ala Leu
85 90 95
Asn Arg Phe Pro Glu Ile Lys Tyr Gly Glu Gly Glu Ile Gly Asp Val
100 105 110
Leu Ser Ala Ile Arg Leu Met Ala Gly Cys Leu Leu Ala Lys Asn Glu
115 120 125
Lys Ser Phe Tyr Lys Phe Phe Leu Arg Gly Phe Gln Phe Asp Lys Asn
130 135 140
Gly Phe Met Met Leu Ser Glu Gly Met Lys Arg Ile Glu Lys Met His
145 150 155 160
Thr Lys Ile Ala Lys Lys Val Phe Gly Gly Cys Lys Ala Ala Pro Leu
165 170 175
Lys Glu Asp Arg Glu Gly Lys Ile Pro Cys Gln Glu Phe His Lys Pro
180 185 190

Ser Ser Tyr Lys Gly Glu Tyr Thr Thr Pro Leu Pro Pro Thr Pro Ala
 195 200 205
 Pro Val Lys Val Leu Pro Pro Leu Leu Pro Tyr Lys Asn Val Lys Asn
 210 215 220
 Lys Pro Val Phe Val Pro Asp Leu Ala Val Gly Glu Ala Lys Lys Pro
 225 230 235 240
 Cys Trp Val His Lys Leu Phe Ser Asp Asp Pro Glu Glu Arg Lys Arg
 245 250 255
 Leu Phe Glu Arg His Gln Ala Gly Arg Arg Asp Ala Leu Met Glu Asp
 260 265 270
 Tyr Gly Val Ile Pro Asn Asn Asp Asn Glu Ala Glu Asp Thr Glu Arg
 275 280 285
 Phe Val Ser Asn Ala Leu Glu Tyr Gln Ala Gln Met Leu Glu Leu Leu
 290 295 300
 Asp Thr Ala Asn Met Pro Pro Pro Ala Ser Thr Pro Val Arg Arg Gly
 305 310 315 320
 Arg Thr Arg Ile Val Arg Asp Tyr Asp Asp Val Pro Ser Pro Tyr Ser
 325 330 335
 Ser Pro Leu His Thr Pro Phe Asp Ala Pro Asn Val Asn Leu Asn Pro
 340 345 350
 Gly Ser Gly Arg Met Val Asp Arg Val Arg Asp Gly Arg Arg Asn Thr
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 Ser Arg Arg Thr Ser Ala Val Met Ala Arg Arg Ile Asn Gln Leu Gln
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<211> 3796

<212> DNA

<213> SHRIMP

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<210> 105

<211> 1255

<212> PRT

<213> SHRIMP

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Glu Arg Leu Lys Thr Ser Lys Ile Arg Leu Asn Lys Ala Leu Ser Asp
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Ile Val Glu Ala Thr Asn Glu Arg Val Asp Ala Leu Lys Glu Asn Gln
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Lys Cys Ser Ile Thr Pro Ser Val Pro Thr Ala Ile Ile Gly Ala His

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Gln Leu Phe	Ser Arg His Asp Asn Thr Lys Cys Val Gly Ala Glu Ile	190
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Cys Val Lys	Gly Asn Glu Lys Asn Lys Phe Val Asn Lys Leu Val Val	205
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Lys Lys Leu	Pro Asn Ala Pro Ser Ser Ser Thr Val Leu Glu Ile	220
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Cys Phe Phe Asp Arg Ile Glu Ile Val Phe Ser Asp Gln Ser Asp Ser					
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Val Lys Gly Ile Asp Phe Val Val Lys Ser Gln Asp Thr Asn Ile Gly					
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<212> DNA

<213> SHRIMP

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<212> PRT
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Glu	Gln	Gly	Lys	Glu	Ser	Leu	Lys	Glu	Tyr	Leu	Asp	Tyr	Asn	Gly	Gln
				85					90					95	
Val	Met	Glu	Ile	Tyr	Ile	Ala	Glu	Trp	Leu	Arg	Gln	Arg	Pro	Leu	Ala
			100					105					110		
Phe	His	Val	Phe	Thr	Tyr	Thr	Asp	Glu	Ala	Val	Lys	Ser	Gly	Phe	Leu
		115					120					125			
Asn	Glu	Glu	Asp	Leu	Asp	Met	Asp	Thr	Ala	Thr	Lys	Trp	Met	Ala	Glu
	130					135					140				
Ile	Ile	Arg	Glu	Lys	Arg	Gly	Asn	Ile	Gln	Glu	Ile	Lys	Val	Thr	Pro
145					150					155					160
Arg	Val	Val	Phe	Asn	Gly	Asn	Val	Cys	Ser	Ala	Cys	Phe	Ser	Asn	Thr
				165					170					175	
Lys	Arg	Asn	Leu	Tyr	Asn	Phe	Gly	Thr	Asn	Tyr	Asn	Asn	Val	Val	His
			180					185					190		
Cys	Asp	Leu	Leu	Cys	Pro	Phe	Ala	Arg	His	Arg	Ile	Val	His	Phe	Leu
		195					200					205			

<210> 114
<211> 375
<212> DNA
<213> SHRIMP

<400> 114

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agactgattc	aaagaattaa	tgatttggaa	tcagaaattg	aaaataaaac	tgaattatgt	120
gaaaaaatca	atgagcagat	gaaaaataca	caactaaaat	atgataaatg	tttcgtagag	180
gaggagacgg	aaaaattccg	caagatggag	gaaagagtta	aatacctcaa	agagcaggga	240
atccctctag	accagaaga	aagacgtaca	atgttggctg	aaattgacaa	gagtaacaaa	300
gagttagatg	cccttcttga	ggaaaatgaa	cgtataataa	agctcattga	tgaagagttg	360
gaaagtatga	aataa					375

<210> 115
<211> 124
<212> PRT
<213> SHRIMP

<400> 115

Met	Trp	Arg	Ser	Cys	Ile	Ser	Asn	Ile	Arg	Glu	Met	Gly	Asp	Asn	Lys
1				5					10					15	
Asp	Tyr	Glu	Thr	Arg	Leu	Ile	Gln	Arg	Ile	Asn	Asp	Leu	Glu	Ser	Glu
			20					25					30		
Ile	Glu	Asn	Lys	Thr	Glu	Leu	Cys	Glu	Lys	Ile	Asn	Glu	Gln	Met	Lys
		35					40					45			
Asn	Thr	Gln	Leu	Lys	Tyr	Asp	Lys	Cys	Phe	Val	Glu	Glu	Glu	Thr	Glu
	50					55					60				
Lys	Phe	Arg	Lys	Met	Glu	Glu	Arg	Val	Lys	Tyr	Leu	Lys	Glu	Gln	Gly

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65          70          75          80
Ile Pro Leu Asp Pro Glu Glu Arg Arg Thr Met Leu Ala Glu Ile Asp
      85          90          95
Lys Ser Asn Lys Glu Leu Asp Ala Leu Leu Glu Glu Asn Glu Arg Ile
      100        105        110
Ile Lys Leu Ile Asp Glu Glu Leu Glu Ser Met Lys
      115        120

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<210> 116
 <211> 252
 <212> DNA
 <213> SHRIMP

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<400> 116
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cgaatccttc aacaaaaaga gaagggaaac cctctagacc cagaagaaag acttgatttg 120
tcggctgata ttgataggag tatgaaagag attgatgatt gtctcgagga aataaaccat 180
atagaattat ccattgatac attattggat gaatgtgaaa acttgcatta tggctcttcaa 240
acaactaaat aa                                     252

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<210> 117
 <211> 83
 <212> PRT
 <213> SHRIMP

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<400> 117
Met Gln Lys Lys Tyr Asp Lys Leu Phe Glu Asp Asp Lys Arg Phe Arg
  1          5          10          15
Glu Ile Glu Glu Arg Ile Leu Gln Gln Lys Glu Lys Gly Asn Pro Leu
      20          25          30
Asp Pro Glu Glu Arg Leu Val Leu Ser Ala Asp Ile Asp Arg Ser Met
      35          40          45
Lys Glu Ile Asp Asp Cys Leu Glu Glu Ile Asn His Ile Glu Leu Ser
      50          55          60
Ile Asp Thr Leu Leu Asp Glu Cys Glu Asn Leu His Tyr Gly Leu Gln
      65          70          75          80
Thr Thr Lys

```

<210> 118
 <211> 2253
 <212> DNA
 <213> SHRIMP

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<400> 118
atggaaaaaa agactgagac ggctgcaaca acagaaaaag acccagaacc gtctgtcagt 60
aaaagggtcca gaaataaaga acccaaaaaca acttctactg ttacacttc tgtaaagtgt 120
taccttttctt ccataatcaa gagtgaaagt agtagaagta atgtcacctc aaccaaagaa 180
aggtttgagg agagggtgtaa atccgtaagc aagatgatgg tcaaaggttc actgtttttg 240
aggtttagtag tggacgagtg tctgagacgt tacaaccatc tagaagacga aatcgataaa 300
tggccagata tgacgaagga taactttttac gtccaattgt tgaggaaggg tttagacaag 360
aagaaattga aagaaggatc tacacatcct gttgtagaag atgtttggaa ttcccccatc 420
gtccaagaaa cattcctatc ccagcaagga gaaggaaata atcccataaa gagacatctc 480
atggatttca ataccatcac ctacgccgcc aaacaactaa aaacttgctt cgaaacaaac 540
ctacgcaccc atttccggac acgacaacag agggccatat ctggatgggt agctgaaaac 600
gggttcgata aaaagtatac gaaactcgta caacactgga taattggatg tacctacaag 660
agtgattggg tggacagtgg tgatttggaagg gggtaaaaag aaggaacgaa aaatttcgtg 720
actcttcata ggaaacattt atgtgttatt agtgataaga agaattgtac aatttcctat 780
tcacctgaag agaaatatcc gataccctca atactaaatt attacaagtt tctacaaaca 840

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gagtatccac aaaacaagaa aatacagaaa atgatatgtt tcccaaaaca caaactaaag 900
atacactatt gtacgtttga ccaaacgacc attcaaggaa tttgtaaaga tttgggagtg 960
tggaaggata tggaagaacg acacaaacaa tcagaagata tactttacaa gcaaggatgg 1020
tacctattat tcgacgttaa aaagattaag aaattgcgtc caaactggaa ctttctactct 1080
atccagacgg acggcgaagg cgtctctgta ctattttcca gagaagtgga agaagtagag 1140
actgtttcca agaaaagtaa gaaaaataaa aaacctagag gagatgagga taggagaaat 1200
taccgcacca ctaatgccaa gtacgtagtg ggtgtagatc cggaagaac taatgtcgtt 1260
tcctgttcgg tatttgatac ccgtcaaaaa agggtagtga gaaaacacag aatgactgcg 1320
aaacaatact atcaagaatc ttggatgaca gatagaagaa aggcaaacga aacgtacaag 1380
aagaacaata aagagtacaa agaggcgtta gaggaataaa ctaggtacga taatggcgaa 1440
gaaattataa atgatggtaa cggtgatact tctacacca ctaaaaaatt cgaagcttac 1500
ttgaaggtag tgaacgagca ctacaggtta ctgtggaacg aaaagggaaa gaaaaagtac 1560
aggaaaaatg ccatgaaagt atactctaga aaacaaaagt gcatatctaa ctttatagat 1620
gaattaatcc ctaaaaggga taaaattgaa gattaccaca ttgcttttgg ggatgcgaaa 1680
tttgctgca cggaagagg tgagcaatac gcatcacctg ccaggatttt cgccaagaag 1740
ataaaggaaa gagtcggagg tgataagagg tttactttcg tggacgagaa atatacgtca 1800
aaagtatgcc atcgctgcaa tcaaccttta aatatgctgg agaaggattg tttttcaccg 1860
aataagaaaa gaaaaccgcc gacaatagta acaaccacaa caacaacaac aacagaagaa 1920
gacgaagaaa atggaaaatg gaagaaggct acacctctca gagaaaatag agataccaga 1980
agatgctcgt ccgaaaagac gcaattcggt tacagttcaa accgaaaagt atcgacagga 2040
gatatctcta tggaaacgcc agtaccttct tccacttctt cttccttttg tactcctact 2100
tccattacat gtgtcttggg aggaaaattc gtcgacaggg acttcaatgc aagcaccaat 2160
attgttcata aatttctagg gttttgggat aaaaagttaa tggaaaagaa agacaagatg 2220
ccgttgaagt atcactttat tcgagttgcc tga 2253

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<210> 119

<211> 746

<212> PRT

<213> SHRIMP

<400> 119

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Pro Ser Val Ser Lys Arg Ser Arg Asn Lys Glu Pro Lys Thr Thr Ser
20     25     30
Thr Val Tyr Thr Ser Val Lys Cys Tyr Leu Ser Ser Ile Ile Lys Ser
35     40     45
Glu Ser Ser Arg Ser Asn Val Thr Ser Thr Lys Glu Arg Phe Glu Glu
50     55     60
Arg Cys Lys Ser Val Ser Lys Met Met Val Lys Gly Ser Leu Phe Leu
65     70     75     80
Arg Leu Val Val Asp Glu Cys Leu Arg Arg Tyr Asn His Leu Glu Asp
85     90     95
Glu Ile Asp Lys Trp Pro Asp Met Thr Lys Asp Asn Phe Tyr Val Gln
100    105    110
Leu Leu Arg Lys Gly Leu Asp Lys Lys Lys Leu Lys Glu Gly Ser Thr
115    120    125
His Pro Val Val Glu Asp Val Trp Asn Ser Pro Ile Val Gln Glu Thr
130    135    140
Phe Leu Ser Gln Gln Gly Glu Gly Asn Asn Pro Ile Lys Arg His Leu
145    150    155    160
Met Asp Phe Asn Thr Ile Thr Tyr Ala Ala Lys Gln Leu Lys Thr Cys
165    170    175
Phe Glu Thr Asn Leu Arg Thr His Phe Arg Thr Arg Gln Gln Arg Ala
180    185    190
Ile Ser Gly Trp Leu Ala Glu Asn Gly Phe Asp Lys Lys Tyr Thr Lys
195    200    205
Leu Val Gln His Trp Ile Ile Gly Cys Thr Tyr Lys Ser Asp Trp Val
210    215    220
Asp Ser Gly Asp Leu Glu Arg Val Lys Glu Gly Thr Lys Asn Phe Val
225    230    235    240

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Thr	Leu	His	Arg	Lys	His	Leu	Cys	Val	Ile	Ser	Asp	Lys	Lys	Asn	Gly
				245					250					255	
Thr	Ile	Ser	Tyr	Ser	Pro	Glu	Glu	Lys	Tyr	Pro	Ile	Pro	Ser	Ile	Leu
			260					265					270		
Asn	Tyr	Tyr	Lys	Phe	Leu	Gln	Thr	Glu	Tyr	Pro	Gln	Asn	Lys	Lys	Ile
		275					280					285			
Gln	Lys	Met	Ile	Val	Val	Pro	Lys	His	Lys	Leu	Lys	Ile	His	Tyr	Cys
	290					295					300				
Thr	Phe	Asp	Gln	Thr	Thr	Ile	Gln	Gly	Ile	Cys	Lys	Asp	Leu	Gly	Val
305					310					315					320
Trp	Lys	Asp	Met	Glu	Glu	Arg	His	Lys	Gln	Ser	Glu	Asp	Ile	Leu	Tyr
			325						330					335	
Lys	Gln	Gly	Trp	Tyr	Leu	Leu	Phe	Asp	Val	Lys	Lys	Ile	Lys	Lys	Leu
			340					345					350		
Arg	Pro	Asn	Trp	Asn	Phe	His	Ser	Ile	Gln	Thr	Asp	Gly	Glu	Gly	Val
		355					360					365			
Ser	Val	Leu	Phe	Ser	Arg	Glu	Val	Glu	Glu	Val	Glu	Thr	Val	Ser	Lys
	370					375					380				
Lys	Ser	Lys	Lys	Asn	Lys	Pro	Arg	Gly	Asp	Glu	Asp	Arg	Arg	Arg	Asn
385					390				395						400
Tyr	Pro	Pro	Thr	Asn	Ala	Lys	Tyr	Val	Val	Gly	Val	Asp	Pro	Gly	Arg
				405					410					415	
Thr	Asn	Val	Val	Ser	Cys	Ser	Val	Phe	Asp	Thr	Arg	Gln	Lys	Arg	Val
			420					425					430		
Val	Arg	Lys	His	Arg	Met	Thr	Ala	Lys	Gln	Tyr	Tyr	Gln	Glu	Ser	Trp
		435					440					445			
Met	Thr	Asp	Arg	Arg	Lys	Ala	Asn	Glu	Thr	Tyr	Lys	Lys	Asn	Asn	Lys
	450					455					460				
Glu	Tyr	Lys	Glu	Ala	Leu	Glu	Glu	Ile	Thr	Arg	Tyr	Asp	Asn	Gly	Glu
465					470					475					480
Glu	Ile	Ile	Asn	Asp	Gly	Asn	Gly	Asp	Thr	Ser	Thr	Pro	Thr	Lys	Lys
				485					490					495	
Phe	Glu	Ala	Tyr	Leu	Lys	Val	Val	Asn	Glu	His	Tyr	Arg	Leu	Leu	Trp
			500					505					510		
Asn	Glu	Lys	Gly	Lys	Lys	Lys	Tyr	Arg	Lys	Asn	Ala	Met	Lys	Val	Tyr
		515					520					525			
Ser	Arg	Lys	Gln	Lys	Cys	Ile	Ser	Asn	Phe	Ile	Asp	Glu	Leu	Ile	Pro
	530					535					540				
Lys	Arg	Asp	Lys	Ile	Glu	Asp	Tyr	His	Ile	Ala	Phe	Gly	Asp	Ala	Lys
545					550					555					560
Phe	Ala	Cys	Thr	Gly	Arg	Gly	Glu	Gln	Tyr	Asp	Ala	Arg	Ile	Phe	Ala
				565					570					575	
Lys	Lys	Ile	Lys	Glu	Arg	Val	Gly	Gly	Asp	Lys	Arg	Phe	Thr	Phe	Val
			580					585					590		
Asp	Glu	Lys	Tyr	Thr	Ser	Lys	Val	Cys	His	Arg	Cys	Asn	Gln	Pro	Leu
		595					600					605			
Asn	Met	Leu	Glu	Lys	Asp	Cys	Phe	Ser	Pro	Asn	Lys	Lys	Arg	Lys	Pro
	610					615					620				
Pro	Thr	Ile	Val	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Glu	Asp	Glu
625					630					635					640
Glu	Asn	Gly	Lys	Trp	Lys	Lys	Ala	Thr	Pro	Leu	Arg	Glu	Asn	Arg	Asp
				645					650					655	
Thr	Arg	Arg	Cys	Ser	Ser	Glu	Lys	Thr	Gln	Phe	Gly	Tyr	Ser	Ser	Asn
			660					665					670		
Arg	Lys	Val	Ser	Thr	Gly	Asp	Ile	Ser	Met	Pro	Val	Pro	Ser	Ser	Thr
		675					680					685			
Ser	Ser	Ser	Phe	Cys	Thr	Pro	Thr	Ser	Ile	Thr	Cys	Val	Leu	Gly	Gly
	690					695					700				
Lys	Phe	Val	Asp	Arg	Asp	Phe	Asn	Ala	Ser	Thr	Asn	Ile	Val	His	Lys
705					710					715					720
Phe	Leu	Gly	Phe	Trp	Asp	Lys	Lys	Leu	Met	Glu	Lys	Lys	Asp	Lys	Met

Pro Leu Lys Tyr His Phe Ile Arg Val Ala
 740 745 735

<210> 120
 <211> 411
 <212> DNA
 <213> SHRIMP

<400> 120
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 aaaaggtctc ataaaactct ttacttgtca aatagaactg aaagacatgc ccagatacaa 120
 aagcagatcg aagagttaca tcacaaaaca aataagcaat ttgaacaggc tcaaaagggtc 180
 ctcgacaaaa acgaagagcg aaagaagcat cagcaacagc aacaaataat aattcctcta 240
 gacccagaag aaagacgtgc aatattggct gaaatcgata aacacatgaa agagattgat 300
 ggtttcatcg aggaaagtga acgtctaggt ttactttag atgcagaaat caataacttg 360
 gaagaaaagg aggttgaaga ggaacatctt ttgaaacaaa aagaagacta a 411

<210> 121
 <211> 134
 <212> PRT
 <213> SHRIMP

<400> 121
 Met Gly Asn Ser Glu Ser Arg Ser Ser Gly Ile Glu Ile Val His Lys
 1 5 10 15
 Asn Gly Ala Pro Lys Arg Ser His Lys Thr Leu Tyr Leu Ser Asn Arg
 20 25 30
 Thr Glu Arg His Ala Gln Ile Gln Lys Gln Ile Glu Glu Leu His His
 35 40 45
 Lys Thr Asn Lys Gln Phe Glu Gln Ala Gln Lys Val Leu Asp Lys Asn
 50 55 60
 Glu Glu Arg Lys Lys His Gln Gln Gln Gln Gln Ile Ile Ile Pro Leu
 65 70 75 80
 Asp Pro Glu Glu Arg Arg Ala Ile Leu Ala Glu Ile Asp Lys His Met
 85 90 95
 Lys Glu Ile Asp Gly Phe Ile Glu Glu Ser Leu Gly Leu Leu Val Asp
 100 105 110
 Ala Glu Ile Asn Asn Leu Glu Glu Lys Glu Val Glu Glu Glu His Leu
 115 120 125
 Leu Lys Gln Lys Glu Asp
 130

<210> 122
 <211> 2772
 <212> DNA
 <213> SHRIMP

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 aaggctctgg ctacccaga tctggtggac aagattaccc agaatgtga cgagacagga 120
 agaaaccaga agtgcccat ccagtttctg gccgacatct cgcacctgat ccaaggagaa 180
 agaaatggag gaaatctggt ccctttgcac ccgttcaaga accaaccaca tctggaacca 240
 agaattagtgg gaagtcttca cgggagaaca ttggacaatg acattgaaga atcatactgt 300
 tattttgtca aggatctgta taatggagta ttttcctatg tgaacggcgt caaggagtta 360
 cagggcgttc tggacaagaa aatatctgga tctggatctg gagaatcctc ctcttctaga 420
 gctcccctga tccaataaac tgatgtggat ttgctgtaca ttttcggtac tttggtagtt 480
 cttcccccca gatctaaagc gtaccgagtc atcactgaag ctgttctagc actccccttc 540
 aatgaattca gtaacaactg gcctcctaca aatatcaaag gagcatacgt gtctagagat 600

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ttcaggatgt ttaatctgtt ggccgggttta gatcatatag aaggagaagt tgggggagaa 660
agtgaatggg aatccataca cgcatctgtc gtcaagcgaa tggtcacccat tatgcgcaac 720
aaagctgaga agaaacctcc atcaacatct agaattttta gagtgtatgt ggctgaacca 780
gttaatgatg cagtgcacaa gatccctata cgtgtactca gtaaattatt cggttcaaga 840
ctcgccggta ttctccagaa agtgactctt tattcaatgc taaatcttcc atatctcctg 900
tcttcaaatt ctatagacat caagcaagga gtaaaaggaa ttacattatc tataccatct 960
gcaagaaaat tgggattcta ttactccaa aaggatacaa cattacaatc ttccctatca 1020
caagatgttg ccgactgcat agtttcaatc aacgctggta ttattgggtg tgatttctct 1080
gaaaaaatac gacagtgcac tgaggagaaa aacaagccag aaaactgttg tatgtgcttt 1140
tgtgaaattg acaagacgcc cgatttttct tatagtgaac atgtggcaag gcacaatttc 1200
ttccccgtcc acgcattctc ctcatcacat gatgacaagt gttgtggagc aaagatttgt 1260
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gaaatgggtg atgtaactcc cctcttaatt aatcttaccg agattgttga ttcggaagag 1740
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atagcgctag ccaactggag aaagagtggg gaattgcccc aaaatatgtt tgatttacta 1980
gaaggggtaa atgccgtact ttatagaggg gacagtttct tgttacgtgc gataaactac 2040
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gctgattcta atcatttgtt ggagaaacac aggattgttt atagtaactg tgttagggtt 2640
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gctaagaaat aa 2772

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<210> 123

<211> 919

<212> PRT

<213> SHRIMP

<400> 123

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Met Ser Ser Ser Ser Ser Ser Ser Phe Ser Phe Arg Ile Ser Thr Tyr
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Gln Thr Phe Leu Lys Ala His Pro Asp Leu Val Asp Lys Ile Thr Gln
          20          25          30
Lys Cys Asp Glu Thr Gly Arg Asn Gln Lys Cys Pro Ile Gln Phe Leu
          35          40          45
Ala Asp Ile Ser His Leu Ile Gln Gly Glu Arg Asn Gly Gly Asn Leu
          50          55          60
Phe Pro Leu His Pro Phe Lys Asn Gln Pro His Leu Glu Pro Arg Ile
          65          70          75          80
Val Gly Ser Leu His Gly Arg Thr Leu Asp Asn Asp Ile Glu Glu Ser
          85          90          95
Tyr Cys Tyr Phe Val Lys Asp Leu Tyr Asn Gly Val Phe Ser Tyr Val
          100          105          110
Asn Gly Val Lys Glu Leu Gln Gly Val Leu Asp Lys Lys Ile Ser Gly
          115          120          125
Ser Gly Ser Gly Glu Ser Ser Ser Ser Arg Ala Pro Leu Ile Pro Ile

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130	135	140
Thr Asp Val Asp Leu Leu Tyr Ile Phe Gly Thr Leu Val Val Leu Pro		
145	150	155
Pro Arg Ser Lys Ala Tyr Arg Val Ile Thr Glu Ala Val Leu Ala Leu		160
	165	170
Pro Phe Asn Glu Phe Ser Asn Asn Trp Pro Pro Thr Asn Ile Lys Gly		175
	180	185
Ala Tyr Val Ser Arg Asp Phe Arg Met Phe Asn Leu Leu Ala Gly Leu		190
	195	200
Asp His Ile Glu Gly Glu Val Gly Gly Glu Ser Glu Trp Glu Ser Ile		205
	210	215
His Ala Ser Val Val Lys Arg Met Val Thr Ile Met Arg Asn Lys Ala		220
	225	230
Glu Lys Lys Pro Pro Ser Thr Ser Arg Ile Phe Arg Val Tyr Val Ala		235
	245	250
Glu Pro Val Asn Asp Ala Val Thr Lys Ile Pro Ile Arg Val Leu Ser		255
	260	265
Lys Leu Phe Gly Ser Arg Leu Ala Gly Ile Leu Gln Lys Val Tyr Ser		270
	275	280
Tyr Ser Met Leu Asn Leu Pro Tyr Leu Leu Ser Ser Asn Ser Ile Asp		285
	290	295
Ile Lys Gln Gly Val Lys Gly Ile Thr Leu Ser Ile Pro Ser Ala Arg		300
	305	310
Lys Leu Gly Phe Tyr Leu Leu Gln Lys Asp Thr Thr Leu Gln Ser Ser		315
	325	330
Leu Ser Gln Asp Val Ala Asp Cys Ile Val Ser Ile Asn Ala Gly Ile		335
	340	345
Ile Gly Asp Asp Phe Ser Glu Lys Ile Arg Gln Cys Ile Glu Glu Lys		350
	355	360
Asn Lys Pro Glu Asn Cys Cys Met Cys Phe Cys Glu Ile Asp Lys Thr		365
	370	375
Pro Asp Phe Ser Tyr Ser Glu His Val Ala Arg His Asn Phe Phe Pro		380
	385	390
Val His Ala Phe Ser Ser Ser His Asp Asp Lys Cys Cys Gly Ala Lys		395
	405	410
Ile Cys Ser Glu Cys Ile Phe Pro Tyr Ile Ile Ser Leu Tyr Glu Lys		415
	420	425
Met Thr Gly Val Ala Gly Val Lys Val Val Asp Leu Phe Gln Cys Pro		430
	435	440
Gly Cys Lys Ser Gly Met Leu Asn Leu Lys Gly Arg Cys Tyr Glu Phe		445
	450	455
Ser Asn Leu Cys Lys Arg Met Ile Leu Pro Tyr Thr Ser Thr His Cys		460
	465	470
Ser Ser Leu Phe Asp Ala Thr Ile Asn Arg Ala Glu Ala Cys Phe Tyr		475
	485	490
Ser Leu Glu Phe Leu Gln Tyr Asp Phe Glu Thr Ala Arg Arg Ile Ala		495
	500	505
His Gly Ala Lys Asp Ile Pro His Val Tyr Asn Lys Val Val Lys Asn		510
	515	520
Val Lys Asp Leu Asp Arg Leu Cys Ala Leu Tyr Cys Tyr Lys Cys Val		525
	530	535
Ser Pro Val Val Cys Asp Glu Pro Asn Glu Ser Thr Asp Tyr Glu Met		540
	545	550
Val Asp Val Thr Pro Pro Leu Ile Asn Leu Thr Glu Ile Val Asp Ser		555
	565	570
Glu Glu Tyr Asp Asp Gly Pro Gly Asn His Met Trp Pro Ala Lys Phe		575
	580	585
Thr Cys Asn Phe Ile Ala Gly Ser Ser Gly Glu Thr Pro Thr Ile Ser		590
	595	600
Thr Cys Arg Asp Ala Val Thr Phe Leu Gly Arg Ala Pro Arg Lys Lys		605
	610	615
		620

Met Ala Gly Trp Asp Asp Gln Ser Ala Val Gly Gln Ala Ile Ile Ala
625 630 635 640
Asn Trp Arg Lys Ser Gly Glu Leu Pro Lys Asn Met Phe Asp Leu Leu
645 650 655
Glu Gly Val Asn Ala Val Leu Tyr Arg Gly Asp Ser Phe Leu Leu Arg
660 665 670
Ala Ile Asn Tyr Pro Cys Val Ile Gly Arg Ser Met Ser Pro Ser Leu
675 680 685
Glu Leu Val Lys Arg Lys Val Asn Lys Ile Ala Leu Ile Lys Ala Phe
690 695 700
Phe His Glu Lys Arg Val Arg Pro Asp Ala Ser Lys Lys Leu Leu Glu
705 710 715 720
Trp Ala Glu Leu Leu Val Lys Ser Tyr Leu Met Glu Val Leu Leu Gln
725 730 735
Thr Pro Glu Cys Val Ile His Arg Ala His Ser Phe Val Gly Lys Thr
740 745 750
Leu Leu Ile Thr Asp Glu Leu Val His Met Arg Pro Asp Asp Ala Thr
755 760 765
Arg Asn Ala Tyr Ile Gln Asn Leu Asn Ala Ala Arg Gln Asn Ala Ala
770 775 780
Ala Ala Ala Ser Phe Ser Gly Ser Leu Pro Lys Pro Glu Phe Val Pro
785 790 795 800
Cys Lys Glu Arg Thr Ile Glu Trp Met Tyr Glu Lys Asp Asn Asp Asp
805 810 815
Val Arg Val Val Asn Cys Pro Ser Cys Lys Lys Ala Ile Gln Lys Tyr
820 825 830
Gly Gly Cys Val Asn Val Phe Cys Glu Cys Gly Thr Asn Met Cys Trp
835 840 845
Ile Cys Glu Glu Lys Val Ser Pro Ala Asp Ser Asn His Cys Val Glu
850 855 860
Lys His Arg Ile Val Tyr Ser Asn Cys Val Arg Val Lys Tyr Ala Leu
865 870 875 880
Glu Ser Met Tyr Gly Phe Glu Ile Cys Thr Met Lys Asn Val Glu Glu
885 890 895
Gly Val Lys Asn Tyr Tyr Val Met Glu Asn Gly Phe Phe Phe Asp Val
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Gln Glu Met Val Ala Lys Lys
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<210> 124

<211> 1536

<212> DNA

<213> SHRIMP

<400> 124

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gtccacctgg agtgtctttt cacctggaga tttgaagagc atatggtgaa tgaaaatcac 180
ctgttatgtc ccatgtgtag ggcctatata cccctgtgtt ggttcttccg taaagtgtat 240
gaagaggtgt acaagtatgc ctcttttcac tcatttttgt tgtctgctga ctatgttaat 300
gatgaagggtg taaaggatac ccttaataag atgtcaacta ttctagcacc tactttcttt 360
gtccccaatg ccaaagggtg taatgagaat gaggatgttt atatggagag ggcttatacc 420
aagttgagtt tcatgcttga aactctatct agacaggaaa tgcattgcatt cagtgaagag 480
acccttgaag ataactatga ggcagcttta atgggtaaat tcaaggatat ccccccttat 540
gaatatgaag gtgaatggct taagtatgta gctccaata ctattgacat tactcaatgc 600
ttgagtaatg atgatgatga tgatgaaggt gataataatg tctcccttag tttgttgtct 660
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gaggtagatg ataatgatga ctcagagtca cttcctgact tgactgttcc ccctagaagt 780
aacaatatta cctttgatac tattagtggg attagtagtt cactttatga tggttaatgat 840
gatgatgatg atgatgacac aatgtctttg cctgacttga atatgcctag tgcttctacg 900

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aatcagccct ctacttcctc aggaagtagt agtagtagta gtaacagtag aaagaggcca 1080
aggtatgggc gtgacgagga caggatgtct aatatttcct ctgagagtaa gagactgtgt 1140
gtagatgtca agaggtatat gtgtagactc gataatattg atgaggagta taatgagatt 1200
gccaataggt atctggctga actttctgct cttagagaaa ggagacagga aactgagaat 1260
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<210> 125

<211> 509

<212> PRT

<213> SHRIMP

<400> 125

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Met Ala Glu Thr Val Ala Val Asp Glu Val Pro Thr Cys Pro Ile Cys
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20     25     30
Gly Met Pro Cys Cys Arg Lys Ser Val His Leu Glu Cys Leu Phe Thr
35     40     45
Trp Arg Phe Glu Glu His Met Val Asn Glu Asn His Leu Leu Cys Pro
50     55     60
Met Cys Arg Ala Tyr Ile Pro Pro Val Trp Phe Phe Arg Lys Val Tyr
65     70     75     80
Glu Glu Val Tyr Lys Tyr Ala Ser Phe His Ser Phe Leu Leu Ser Ala
85     90     95
Asp Tyr Val Asn Asp Glu Gly Val Lys Asp Thr Leu Asn Lys Met Ser
100    105    110
Thr Ile Leu Ala Pro Thr Phe Phe Val Pro Asn Ala Lys Gly Val Asn
115    120    125
Glu Asn Glu Asp Val Tyr Met Glu Arg Ala Tyr Thr Lys Leu Ser Phe
130    135    140
Met Leu Glu Thr Leu Ser Arg Gln Glu Met His Ala Phe Ser Glu Glu
145    150    155    160
Thr Phe Glu Asp Asn His Glu Ala Ala Leu Met Gly Lys Phe Lys Asp
165    170    175
Ile Pro Pro Tyr Glu Tyr Glu Gly Glu Trp Leu Lys Tyr Val Ala Pro
180    185    190
Asn Thr Ile Asp Ile Thr Gln Cys Leu Ser Asn Asp Asp Asp Asp
195    200    205
Glu Gly Asp Asn Asn Val Ser Pro Ser Leu Leu Ser Gly Val Thr Ser
210    215    220
Phe Asn Phe Ile Glu Asp Asp Glu Asp Thr Val Val Phe Val Pro Pro
225    230    235    240
Glu Val Asp Asp Asn Asp Asp Ser Glu Ser Leu Pro Asp Leu Thr Val
245    250    255
Pro Pro Arg Ser Asn Asn Ile Thr Phe Asp Thr Ile Ser Gly Ile Ser
260    265    270
Ser Ser Leu Tyr Asp Val Asn Asp Asp Asp Asp Asp Asp Thr Met
275    280    285
Ser Leu Pro Asp Leu Asn Met Pro Ser Ala Ser Thr Ser Ser Ala Pro
290    295    300
Thr Ser Ser Ala Pro Thr Ser Thr Ser Leu Asn Ile Asn Val Asn Leu
305    310    315    320
Cys Phe Asn Val Asp Ser Asp Ser Asp Asp Glu Glu Val Ile Pro Ser
325    330    335
Ser Ser Ser Val Asn Gln Pro Ser Thr Ser Ser Gly Ser Ser Ser Ser

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<210> 127

<211> 575
 <212> PRT
 <213> SHRIMP

<400> 127

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His	His	His	Gln	Tyr	Val	Tyr	His	Gln	Gly	Asn	Lys	Lys	Arg	Pro	
			20				25					30			
Val	Glu	Glu	Tyr	Asn	Asn	Asn	Asn	Tyr	Ala	Ser	Gly	Ser	Thr	Ser	Glu
			35				40					45			
Ala	Thr	Thr	Val	Pro	Ala	Tyr	Asn	Asn	Asn	Asn	Asn	Asn	Ile	Thr	Ile
			50				55					60			
Lys	Thr	Trp	Asp	Asp	Val	Ile	Asn	Leu	Ser	Ile	Thr	Pro	Pro	Pro	Pro
65					70					75					80
Lys	Arg	Phe	Lys	Lys	Ser	Glu	Val	Ala	Pro	Ser	Pro	Pro	Thr	Thr	Arg
				85					90					95	
Thr	Phe	Ser	Asn	Val	Cys	Ala	Ser	Lys	Val	Ile	Arg	Gln	Cys	Lys	Arg
			100					105					110		
Gln	Tyr	Asn	Glu	Trp	Ile	Glu	Arg	Asp	Ser	Pro	Tyr	Tyr	Phe	Lys	Gly
			115					120				125			
Ile	Glu	Lys	Ser	Cys	Ser	Leu	Glu	Asp	Asn	Tyr	Asp	Thr	Cys	Gln	Gln
			130				135					140			
Leu	Arg	Ile	Gly	His	Arg	Ser	Ile	Val	Lys	Ser	Ser	Lys	Tyr	Val	His
145					150					155					160
Asp	Thr	Cys	Phe	Tyr	Gly	Lys	Asp	Pro	Lys	Val	Gly	Phe	Tyr	Trp	Pro
				165					170					175	
Thr	Ser	Ser	Cys	Asp	Glu	Glu	Met	Arg	Phe	Phe	Asp	Thr	Arg	His	Ile
			180					185					190		
Leu	Lys	Glu	Leu	Ser	Ser	Arg	Asn	Ile	Pro	Ser	Ser	Gln	Ile	Met	Asp
			195				200					205			
Ile	Met	Tyr	Met	Ala	Val	Glu	Val	Phe	Gln	Leu	Pro	Ser	Ser	Ala	Cys
			210				215					220			
Glu	Arg	Ile	Arg	Gln	Lys	Thr	Ser	Thr	Leu	Ile	Lys	Glu	Val	Ser	Asp
225					230					235					240
Gln	Cys	Glu	Asn	Trp	Glu	Asn	Phe	Arg	Lys	Thr	Arg	Cys	Leu	Ser	Asp
				245					250					255	
Leu	Val	Glu	Val	Pro	Glu	Asp	Val	Lys	Asp	Phe	Asn	Thr	Phe	Ile	Cys
			260					265					270		
Pro	Trp	Glu	Thr	Phe	Phe	Glu	Ile	Lys	Tyr	Gly	Val	Tyr	Tyr	Ile	Val
			275				280					285			
Asn	Arg	Gly	Thr	Val	Val	Lys	Phe	Met	Lys	Asp	Met	Asn	Tyr	Glu	Glu
			290			295					300				
Phe	Val	Phe	Glu	Cys	Val	Asn	Gly	Leu	Ser	Val	Tyr	Arg	Lys	Asn	Ile
305					310					315					320
Lys	Gly	Val	Val	Gly	Val	Thr	Gly	Val	Cys	Pro	Gln	Gly	Leu	Cys	Leu
				325					330					335	
Glu	Met	Pro	Phe	Ala	Gly	Ile	Ser	Ile	Asp	Asp	Val	Ile	Arg	Cys	Val
			340					345					350		
Lys	Asp	Ser	Leu	Asp	Gly	Gly	Glu	Tyr	Tyr	Glu	Ser	Arg	Asp	Ala	Arg
			355				360					365			
Leu	Leu	Tyr	Gly	Val	Val	Met	Leu	Gln	Arg	Met	Gly	Arg	Leu	Pro	Glu
			370			375					380				
Val	Lys	Gly	Val	Asp	Thr	Val	Ala	Pro	Ile	Thr	Asp	Ser	Phe	Ile	Ala
385					390					395					400
Arg	Lys	Val	Val	Arg	Ser	Met	Phe	Glu	Lys	Leu	Lys	Val	Asn	Met	Pro
				405					410					415	
Phe	Val	Leu	Ala	Glu	Thr	Cys	Asn	Val	Ile	Thr	Arg	Val	Ala	Asn	Glu
			420					425					430		
Gly	Ile	Ile	Asn	Val	Asp	Ile	Lys	Ala	Asp	Asn	Phe	Val	Ile	Asp	Ser
			435				440					445			

Ile Ser Gly Gln Pro Lys Met Ile Asp Leu Gly Leu Ser Tyr Pro Leu
 450 455 460
 Gly Tyr Cys Tyr Asn Asp Glu Tyr Phe Arg Asn Thr Glu Glu Leu Ile
 465 470 475 480
 Arg Gln Tyr Ile His Thr Pro Pro Glu Phe Phe Arg Gly His Cys Leu
 485 490 495
 Gly Ala Tyr Ser Met Thr Tyr Ser Phe Ser Val Met Ala Ser Ser Ile
 500 505 510
 Asp Val Val Ala Cys Ser Asn Met Glu Gly Pro Ala Phe Asn Leu Met
 515 520 525
 Ser Asn Met His Phe Leu Met Leu Leu Gln Ser Gly Thr Asp Thr Asp
 530 535 540
 Phe Tyr Gln Asn Arg Pro Ser Ile Thr Glu Tyr Ala Met Lys His Ile
 545 550 555 560
 Phe Pro Phe Lys Gly Thr Val Met Asn Leu Phe Lys Val Lys Lys
 565 570 575

<210> 128
 <211> 1200
 <212> DNA
 <213> SHRIMP

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 gaagaattaa acaaggattht actggatagt gtaagaaatc agatcaaatt cgggttcgac 180
 ccaatcactg aaacgttgaa aaattgtata actactcaaa cacttttaca ctcttttctc 240
 aagagtagtc tcctgactct acaagaaaaa tttaatgaat ggggatcaat tcaactagag 300
 aaaggaggac aggaaatggc actgtgtgcg agccttaaaa tcatgggcca aatatcagct 360
 ttaattgaaa ctgcaaagga ggcctcaatg gataataaaa agaagaataa taatgcatgt 420
 gcgaattgcc gggatagtaa gtgttcggcc agtttagtta cattatttaa taaaactatc 480
 gatgaaaagt atgttaagca aaactcttca tcagcctcgg ctcttctggc aaatactttc 540
 acggctggtg caaataaacc acccaaagag tttataacaa aagataatgc acatggcaat 600
 tctgatacta attatacagc catgagtgat aaccttattt gtccaggcaa atactactca 660
 tctgatatta catatgaagt aacaaagcaa gctaaagaac gcataaaaaa taacaataag 720
 aaaatgagac tagcaacagg cgtggaaaatg gtaatgaagg aactagaagc agaaaaataat 780
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 ccttttgccc cttcagctga tattgttgtt gataaaacat cagaaattat gggcagaaca 1080
 cctggctcag aatgggttca ccagagagac aggaatagta aaatggagat acgaaactat 1140
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<210> 129
 <211> 395
 <212> PRT
 <213> SHRIMP

<400> 129
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 Val Leu Lys Asn Ile His Phe Ser Glu Ser Ile Pro Ala Asn Asp Ile
 20 25 30
 Ile Ser Phe Pro Ser Ser Asp Thr Glu Glu Leu Asn Lys Asp Leu Leu
 35 40 45
 Asp Ser Val Arg Asn Gln Ile Lys Phe Gly Phe Asp Pro Ile Thr Glu
 50 55 60
 Thr Leu Lys Asn Cys Ile Thr Thr Gln Thr Leu Leu His Ser Phe Leu

65					70					75					80
Lys	Ser	Ser	Leu	Leu	Thr	Leu	Gln	Glu	Lys	Phe	Asn	Glu	Trp	Gly	Ser
				85					90					95	
Ile	Gln	Leu	Glu	Lys	Gly	Gly	Gln	Glu	Met	Ala	Leu	Cys	Ala	Ser	Leu
			100					105					110		
Lys	Ile	Met	Gly	Gln	Ile	Ser	Ala	Leu	Ile	Glu	Thr	Ala	Lys	Glu	Ala
		115					120					125			
Ser	Met	Asp	Asn	Lys	Lys	Lys	Asn	Asn	Asn	Ala	Cys	Ala	Asn	Cys	Arg
		130					135				140				
Asp	Ser	Lys	Cys	Ser	Ala	Ser	Leu	Val	Thr	Leu	Phe	Asn	Lys	Thr	Ile
145					150					155					160
Asp	Glu	Lys	Tyr	Val	Lys	Gln	Asn	Ser	Ser	Ser	Ala	Ser	Ala	Leu	Leu
				165					170					175	
Ala	Asn	Thr	Phe	Thr	Ala	Gly	Ala	Asn	Lys	Pro	Pro	Lys	Glu	Phe	Ile
			180					185					190		
Thr	Lys	Asp	Asn	Ala	His	Gly	Asn	Ser	Asp	Thr	Asn	Tyr	Thr	Ala	Met
		195					200					205			
Ser	Asp	Asn	Leu	Ile	Cys	Pro	Gly	Lys	Tyr	Tyr	Ser	Ser	Asp	Ile	Thr
	210					215					220				
Tyr	Glu	Val	Thr	Lys	Gln	Ala	Lys	Glu	Arg	Ile	Lys	Asn	Asn	Asn	Lys
225					230					235					240
Lys	Met	Arg	Leu	Ala	Thr	Gly	Val	Glu	Met	Val	Met	Lys	Glu	Leu	Glu
				245					250					255	
Ala	Glu	Asn	Asn	Lys	Glu	Gly	Gly	Arg	Val	Glu	Val	Glu	Val	Glu	Gly
			260					265					270		
Val	Glu	Gln	Gln	Pro	Ser	Thr	Ser	Gly	Glu	Glu	Met	Gln	Met	Glu	
		275					280					285			
Ile	Met	Leu	Pro	Thr	Pro	Pro	Pro	Pro	Asp	Leu	Glu	Ser	Leu	Val	Thr
	290					295					300				
Glu	Gly	Val	Asp	Asp	Tyr	Pro	Val	Phe	Ser	Pro	Leu	Pro	Ser	Leu	Leu
305					310					315					320
Ser	Pro	Met	Pro	Asp	Leu	Pro	Ser	Asn	Gly	Asn	Ser	Ala	Leu	Glu	Asp
				325					330					335	
Gly	Gly	Pro	Phe	Ala	Pro	Ser	Ala	Asp	Ile	Val	Val	Asp	Lys	Thr	Ser
			340					345					350		
Glu	Ile	Met	Gly	Arg	Thr	Pro	Gly	Ser	Glu	Trp	Val	His	Gln	Arg	Asp
		355					360					365			
Arg	Asn	Ser	Lys	Met	Glu	Ile	Arg	Asn	Tyr	Gly	Arg	Ser	Gly	Ile	Asn
	370					375					380				
Thr	Gly	Arg	Tyr	Arg	Arg	Asn	Asn	Thr	Val	Leu					
385					390					395					

<210> 130
 <211> 1233
 <212> DNA
 <213> SHRIMP

<400> 130
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 gacaagaaat tttcttccaa ggctctactc ttggcctcta cgccattcc cagtgcagaa 180
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 aaagcgtaaa agattgttgt tactggactt tatgtagatg gggaatatgt ggatgatgtt 300
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 aatagtatgt taatggacaa ggcagaagac gcagacgaaa ttcgttgttg acttattcct 420
 ctaggagagag ggtttaatag agaggctttc aagtttgttg acccagttat cccttggtgc 480
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 atgtttgaag tgggtgaaaca attttcaatc aaacacaaca atagaatctt cactataaat 660
 caagttgatt ttaaagggtga agaaatgaaa atgttctttg ctctctacag cgaagagtta 720

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cttcctttct attcagaaac gggaaaatta ttatctgaga aacacgtctc caaatcattt 780
tctcagttgc ctccacatgt gaccatttct gttttctatt tgcgaaatat ggaagaatac 840
aatactctga tgaaaacaga ttttgggagt tgttttgcac cagctatcaa aatcgacact 900
ggggataatt ttgagttggt tgggatgaac aacaacattc tcgtatccaa agtatgtgtt 960
ggagatgatg cactcgattt gcgtagacga ataatggaac acatttcaga tgcaataggg 1020
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<210> 131
 <211> 404
 <212> PRT
 <213> SHRIMP

<400> 131

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Val	Phe	Phe	Asp	Phe	Ser	Asp	Asn	Thr	Ser	Met	Ser	Asn	Met	Val	Asp
			20					25					30		
Asn	Ile	Arg	His	Arg	Leu	Pro	Met	Asp	Lys	Lys	Phe	Ser	Ser	Lys	Ala
		35					40					45			
Leu	Leu	Leu	Ala	Ser	Thr	Pro	Ile	Pro	Ser	Asp	Glu	Gln	Leu	Ser	Thr
	50				55					60					
Lys	Val	Asn	Lys	Ala	Ile	Phe	Ser	His	Arg	Glu	Thr	Ile	Val	Leu	Ser
65					70				75					80	
Lys	Ala	Leu	Lys	Ile	Val	Val	Thr	Gly	Val	Asp	Gly	Glu	Tyr	Val	Asp
			85					90					95		
Asp	Val	Ile	Cys	Leu	Tyr	Pro	Glu	Lys	His	Thr	Leu	Asn	Gly	Ile	Leu
			100					105					110		
Arg	Tyr	Val	Val	His	Leu	Asn	Met	Met	Leu	Met	Asp	Lys	Ala	Glu	Asp
		115					120					125			
Ala	Asp	Glu	Ile	Arg	Cys	Gly	Leu	Ile	Pro	Leu	Gly	Arg	Gly	Phe	Asn
		130				135					140				
Arg	Glu	Ala	Phe	Lys	Phe	Val	Asp	Pro	Val	Ile	Pro	Cys	Ala	Gly	Tyr
145					150					155					160
Asn	Ile	Leu	Asn	Gly	Tyr	His	Pro	Asp	Asn	Gly	His	Gln	Ile	Ser	Pro
			165					170						175	
Ser	Ser	Thr	Gln	Pro	Gln	Val	Gln	Arg	Arg	Cys	Ala	Val	Lys	Gln	Met
		180					185					190			
Tyr	Lys	Gln	Ile	Asn	Gly	Met	Phe	Glu	Val	Val	Lys	Gln	Phe	Ser	Ile
		195				200					205				
Lys	His	Asn	Asn	Arg	Ile	Phe	Thr	Ile	Asn	Gln	Val	Asp	Phe	Lys	Gly
		210			215					220					
Glu	Glu	Met	Lys	Met	Phe	Phe	Ala	Lys	Glu	Glu	Leu	Leu	Pro	Phe	Tyr
225					230				235						240
Ser	Glu	Thr	Gly	Lys	Leu	Leu	Ser	Glu	Lys	His	Val	Ser	Lys	Ser	Phe
			245					250					255		
Ser	Gln	Leu	Pro	Pro	His	Val	Thr	Ile	Ser	Val	Phe	Tyr	Leu	Arg	Asn
		260					265						270		
Met	Glu	Glu	Tyr	Asn	Thr	Leu	Met	Lys	Thr	Asp	Phe	Gly	Ser	Cys	Phe
		275				280					285				
Ala	Pro	Ala	Ile	Lys	Ile	Asp	Thr	Gly	Asp	Asn	Phe	Glu	Leu	Phe	Gly
		290			295					300					
Met	Asn	Asn	Asn	Ile	Leu	Val	Ser	Lys	Val	Cys	Val	Gly	Asp	Asp	Ala
305					310					315					320
Leu	Asp	Leu	Arg	Arg	Arg	Ile	Met	Glu	His	Asp	Ala	Ile	Gly	Arg	Asn
			325					330					335		
Val	Glu	Leu	Ala	Asp	Asn	Arg	Leu	Asn	Pro	His	Ile	Thr	His	Gly	Lys
		340					345					350			
Ile	Asn	Glu	Gly	Val	Val	Gly	Glu	Trp	Val	Ser	Arg	Phe	Ala	Pro	Cys

355	360	365
Asn Phe Leu Cys Lys Pro Arg Glu Glu Ile Val	Phe Gly Gly Thr Lys	
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 Leu Arg Val Arg Thr Ser Ser Ser Ser Lys Tyr Val Glu Gly Gly Gln
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 Lys Asp Met Val Gly Phe Tyr Glu Ala Ser Lys Arg Val Pro Arg Val
 1425 1430 1435 1440
 Met Arg Arg Val His Val Leu Pro Val Leu Thr Pro Tyr His Gly Gly
 1445 1450 1455
 Phe Glu Ser Cys Ala Pro Thr Ala Ala Gln Ser Ala Cys Thr Arg Gly
 1460 1465 1470
 Val Glu Ile Thr Tyr Ala Asp Phe Met Arg Pro Ser Asp Leu Ser Gly
 1475 1480 1485
 Thr Lys Thr Thr Leu Glu Gly Val Arg Val Lys Gly Pro Glu Pro Phe
 1490 1495 1500
 Asp Asp Leu Ser Thr Leu Tyr Phe Arg Ser Val Gly Gly Pro Asn Leu
 1505 1510 1515 1520
 Arg Lys Phe Ala His His His His Phe Gly Tyr Glu Gly Leu Met Ser
 1525 1530 1535
 Arg Tyr Tyr Tyr Thr Arg Glu Lys Thr Val Ser Val Ser Glu Gly Asp
 1540 1545 1550
 Leu Lys Asp Arg Phe Pro Phe Val Cys Gln Ser Asp Arg Gly Pro Phe
 1555 1560 1565
 Pro Pro Lys Arg Asp Gly Thr Ile Gln Pro Leu Ala Leu Val Asp Met


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ttctacaata ataatggtgc aaacaatgaa tttacttcct cgttactatt tgctatatagtt 3060
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<210> 137

<211> 1156

<212> PRT

<213> SHRIMP

<400> 137

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Met Lys Ile Val Gln Asn Asn Phe Thr Pro Asp Glu Arg Ser Gly Val
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20     25     30
Ile Ala Ala Ala Ile Asp Asp Ser Ala Ala Val Arg Lys Asp Pro Lys
35     40     45
Lys Lys Arg Asn Leu Lys Asn Gly Leu Glu Pro Ala Ser Lys Lys Leu
50     55     60
Ala Lys Asn Ile Glu Arg Ile Ser Ser Glu Glu Leu Lys Arg Val Thr
65     70     75     80
Asp Val Gln Asp Pro Lys Leu Leu His Ser Ile Met Lys Arg Thr Ala
85     90     95
Arg Gln Ile Gly Tyr Asp Ile Gly Asp Asp Ile Ser Pro Gln Ser Ala
100    105    110
Pro Asp Arg Asp Gly Ser Ser Ser Ser Leu Leu Pro Ile Arg Met
115    120    125
Ile Asn Ile Arg Thr Glu Glu Leu Leu Glu Lys Gly Gly Lys Asp Thr
130    135    140
Ile Val Arg Ile His Ile Leu Asp Gly Ile Leu Pro Asp Asn Val Pro
145    150    155    160
Leu Pro Phe Lys Ala Glu Ile Lys Val Asp Leu Val Asp Glu Lys Tyr
165    170    175
Glu Gly Glu Asp Gly Gly Gly Ser Ser Asp Ser Gly Pro Ser Leu Phe
180    185    190
Glu Thr Phe Pro Glu Phe Val Pro Ala Gly Trp Pro Pro Ile Thr Asn
195    200    205
Asp Pro Asn Ala Phe Ser Arg Asn Asn Gly Asn Lys Gln Gln Ala Val
210    215    220
Phe Lys His Val Glu Val Asn Ser Leu Ala Asp Gly Ile Thr Leu Ser
225    230    235    240
Thr Lys Gly Ser Ile Phe Asn Thr Gly Asn Arg Leu Lys Ile Ser Ile
245    250    255
Val Thr Glu Asp Lys Asn Lys Thr Val Leu Phe Asp Ser Gln Val Thr
260    265    270
Ile Ser Ser Pro Ile Pro Lys Ile Thr Glu Val Phe Ala Cys Arg Asn
275    280    285
Val Met Arg Leu Asp Met Pro Lys Ala Ile Asn Tyr Asp Asn Val Glu
290    295    300
Tyr Thr Pro Asp Thr Leu Asn Glu Lys Tyr Val Ser Asp Tyr Pro Ala
305    310    315    320
Asn Phe Pro Arg Leu Ser Arg Gln Ala Glu Ile Asn Leu Ala Ala Lys
325    330    335
Leu Pro Arg Glu Asn Gln Leu Ser Asp Ile Asn Lys Pro Ser Val Ser
340    345    350
Phe Val Tyr Ser Lys Thr Asn Thr Val Asn Thr Pro Val Leu Asn Lys

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		355					360					365			
Val	Leu	Tyr	Asn	Glu	Thr	Leu	Lys	Asn	Met	Glu	Gly	Asn	Glu	Ser	Glu
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Gly	Tyr	Lys	Ile	Leu	Asn	Ala	Thr	Glu	Ile	Thr	His	Leu	Arg	Asn	Pro
385					390					395					400
Ser	Asn	Pro	Ala	Arg	Thr	Phe	Ile	Cys	Val	Ser	Val	Pro	Glu	Ser	Glu
				405					410						415
Ile	Glu	Ala	Gln	Trp	Lys	Met	Leu	Gly	Trp	Ile	Val	Gly	Phe	Lys	Thr
			420					425					430		
Ser	Ser	Asp	Val	Leu	Thr	Thr	Ser	Ser	Gly	Tyr	Asn	Ile	Val	Phe	Pro
		435					440					445			
Ala	Ser	Lys	Val	Thr	Gln	Ser	Asp	Lys	Leu	Phe	Ser	Val	Ile	Ser	Thr
		450					455					460			
Asp	Val	Asn	Ala	Asn	Thr	Asn	Lys	Val	Val	Val	His	Asn	Thr	Pro	Ser
465					470					475					480
Arg	Val	Gly	Cys	Phe	Gly	Ser	Ser	Val	Asn	Phe	Arg	Val	Asp	Ala	Ala
				485					490					495	
Thr	Ala	Pro	Asp	Trp	Pro	Gly	Pro	Thr	Asn	Gly	Pro	Asp	Phe	Phe	Ser
			500					505					510		
Tyr	Gln	Leu	Arg	Pro	Cys	Ile	Ile	Leu	Lys	Thr	Asp	Asn	Asp	Asn	Arg
		515					520					525			
Glu	Pro	Arg	Ile	Thr	Ala	Val	Leu	Ser	Ser	Pro	Ala	Thr	Glu	Tyr	Ala
	530						535					540			
Gly	Glu	Arg	Thr	Thr	Ser	Leu	Leu	Pro	Arg	Ala	Leu	Asn	Val	Ser	Val
545						550				555					560
Gly	Pro	Leu	Thr	Glu	Val	Arg	Gly	Gly	Asp	Ile	Ile	Thr	Pro	Val	Gln
				565					570					575	
Thr	Ala	Leu	Leu	Gly	Gly	Glu	Gln	Pro	Thr	Phe	Lys	Ala	Pro	Ala	Glu
			580					585					590		
Pro	Thr	Lys	Leu	Tyr	Ala	Val	Phe	Pro	Val	Leu	Asp	Ser	His	Asn	Gly
		595					600					605			
Leu	Val	Lys	Ala	Ser	Asp	Asn	Pro	Phe	Gln	Pro	Ile	His	Ser	Ile	Thr
	610					615					620				
Ser	Arg	Asn	Lys	Thr	Thr	Val	Leu	Thr	Val	Ser	Asp	Val	Ile	Val	Asn
625					630					635					640
Asp	Asp	Asp	Asp	Asp	Val	Val	Leu	Glu	Asp	Lys	Ser	Tyr	His	Ile	Thr
				645					650					655	
Val	Ser	Asp	Pro	Val	Ser	Gly	Ser	Ile	Leu	Ala	Lys	Glu	Asn	Val	Leu
			660					665					670		
Ser	Ser	Arg	Ile	Thr	Ser	Arg	Pro	Ile	Phe	Ile	Asp	Gly	Ala	Arg	Asp
		675					680					685			
Asp	Arg	Val	Phe	Ser	Val	Lys	Met	Glu	Val	Phe	Gly	Gly	Asp	Asp	Lys
	690					695					700				
Gly	Ile	Gln	Met	Pro	Phe	Thr	Met	Asp	Gly	His	Phe	Glu	Gly	Gln	Phe
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Ser	Asp	Met	Ser	Val	Pro	Ser	Asn	Glu	Leu	Ala	Ile	Trp	Asn	Asp	Pro
				725					730					735	
Ser	Thr	Phe	Thr	Ala	Pro	Val	Arg	Asp	Thr	Pro	Ala	Thr	Asp	Ile	Thr
			740					745					750		
Asn	Lys	Gly	Ile	Val	Tyr	Cys	Arg	Thr	Thr	Leu	Pro	Pro	Ile	Ser	Asn
		755					760					765			
Arg	Gly	Ile	Arg	Asp	Pro	Phe	Met	Lys	Gln	Thr	Ser	Leu	Val	Pro	Leu
	770					775					780				
Pro	Thr	Ser	Ile	Pro	Glu	Trp	Ala	Phe	Ala	Asp	Tyr	Gly	Gly	Glu	Ile
785					790					795					800
Lys	Tyr	Pro	Arg	His	Ile	Phe	Ile	Ser	Ser	Ile	Arg	Thr	Asn	Asp	Thr
				805					810					815	
Thr	Asn	Ile	Val	Asn	Thr	Asp	Thr	Gln	Thr	Glu	Phe	Ser	Ile	Glu	Asn
			820					825					830		
Trp	Leu	Arg	Glu	Gln	Ile	Asp	Lys	Glu	Gln	Glu	Arg	His	Arg	Gln	Leu
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<211> 204
 <212> PRT
 <213> SHRIMP

<400> 139

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			20					25					30		
Val	Phe	Asn	Thr	Arg	Val	Gly	Arg	Ser	Val	Val	Ala	Asn	Tyr	Asp	Gln
		35					40					45			
Met	Met	Arg	Val	Pro	Ile	Gln	Arg	Arg	Ala	Lys	Val	Met	Ser	Ile	Arg
	50					55					60				
Gly	Glu	Arg	Ser	Tyr	Asn	Thr	Pro	Leu	Gly	Lys	Val	Ala	Met	Lys	Asn
65					70					75					80
Gly	Leu	Ser	Asp	Lys	Asp	Met	Lys	Asp	Val	Ser	Ala	Asp	Leu	Val	Ile
				85					90					95	
Ser	Thr	Val	Thr	Ala	Pro	Arg	Thr	Asp	Pro	Ala	Gly	Thr	Gly	Ala	Glu
			100					105					110		
Asn	Ser	Asn	Met	Thr	Leu	Lys	Ile	Leu	Asn	Asn	Thr	Gly	Val	Asp	Leu
		115					120					125			
Leu	Ile	Asn	Asp	Ile	Thr	Val	Arg	Pro	Thr	Val	Ile	Ala	Gly	Asn	Ile
	130					135					140				
Lys	Gly	Asn	Thr	Met	Ser	Asn	Thr	Tyr	Phe	Ser	Ser	Lys	Asp	Ile	Lys
145					150					155					160
Ser	Ser	Ser	Ser	Lys	Ile	Thr	Leu	Ile	Asp	Val	Cys	Ser	Lys	Phe	Glu
				165					170					175	
Asp	Gly	Ala	Ala	Phe	Glu	Ala	Thr	Met	Asn	Ile	Gly	Phe	Thr	Ser	Lys
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<210> 140
 <211> 2571
 <212> DNA
 <213> SHRIMP

<400> 140

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gaaaaacaaa	ggaagggtgt	tattttcttct	gacgtattcg	gacccacgtg	gttcaataaa	180
acgacagaat	tttttaattc	gggactaaga	ttagccaaag	gacacctatc	taaagatgcc	240
gtcatgagga	gtgtctacag	agatatagaa	ggtgttagag	agcatataat	tgacccctct	300
tggagattga	ccgaaactgc	agcggaagaa	ctatgtgact	ttactttttt	gaaacaagca	360
ccattattga	accttttgaa	tgcccttgag	aatattatgg	acggtgtggt	tagatcagca	420
gctaattctag	ttctttattc	cactagaggt	gatactaatt	aaccttcatg	ggtaattgat	480
tcagaaatgt	tgGCCAACAG	aaacaattca	acggtggccg	atctggcaat	gggacgagca	540
aaaagagcca	ttgctctatt	tctaggatat	actctttgtg	atatttctaag	atggaagcaa	600
tctatcgctt	ctagaatgaa	agagaggggt	ttagatccct	ttgctgccat	gcctcctcac	660
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gtaggttcct	tccatgaagc	tcttttaggg	agggaaatca	tggtactatt	atcagcagcc	900
atcgacgcag	agtacagggc	agtgtgtgcc	aggaccagaa	acgctaaacc	aaatcctttg	960
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acagaaaagg	aaaaagaatg	ggtcgaagag	gaagagagaac	gaattaaaac	tacggatatg	1080
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gttatgttct	ccaactactc	tgttaccgcg	gttcttgatc	ccgactcagc	tgcccgaattt	1320

			260					265					270		
Gly	Phe	Tyr	Pro	Pro	Lys	Val	Gly	Ser	Phe	His	Glu	Ala	Leu	Leu	Gly
		275					280					285			
Arg	Glu	Ile	Met	Val	Leu	Leu	Ser	Ala	Ala	Ile	Asp	Ala	Glu	Tyr	Arg
	290					295					300				
Ala	Val	Leu	Ser	Arg	Thr	Arg	Asn	Ala	Lys	Pro	Asn	Pro	Leu	Thr	Thr
305					310					315					320
Lys	Leu	Asp	Lys	Tyr	Val	Asn	Asn	Pro	His	Leu	Gln	Met	Pro	Ser	Glu
				325					330					335	
Ser	Val	Thr	Glu	Arg	Glu	Lys	Glu	Trp	Val	Glu	Arg	Glu	Arg	Glu	Arg
			340					345					350		
Ile	Lys	Thr	Thr	Asp	Met	Thr	Ala	Glu	Asn	Leu	Phe	Arg	Asp	His	Pro
		355					360					365			
Tyr	Leu	Pro	Lys	Ala	Ile	Asp	Gly	Ile	Leu	Gly	Pro	Lys	Arg	Thr	Pro
	370					375					380				
Thr	Ala	Leu	Gln	Ala	Leu	Gln	Arg	Glu	Tyr	Lys	Arg	Cys	Asn	Lys	Phe
385					390					395					400
Asn	Asp	Ile	Val	Ser	Pro	Glu	Thr	Leu	Glu	Tyr	Phe	Leu	Val	Asn	Asn
				405					410					415	
Arg	Gln	Val	Met	Phe	Ser	Asn	Tyr	Ser	Val	Thr	Arg	Val	Leu	Asp	Pro
			420					425					430		
Asp	Ser	Ala	Ala	Arg	Phe	Ser	Met	Tyr	Val	Leu	Trp	Asn	Ala	Leu	Phe
		435					440					445			
Leu	Cys	Ser	Gly	Gly	Leu	Thr	Gln	Lys	Thr	Asn	Ser	Ser	Ala	Val	Lys
	450					455					460				
Ser	Arg	Leu	Ile	Leu	Gln	Val	Phe	Leu	Lys	Asp	Met	His	Ser	Leu	Phe
465					470					475					480
Val	Cys	Gln	Arg	Cys	Glu	Ser	Gly	Phe	Ile	Thr	Lys	Ser	Leu	Asp	Thr
				485					490					495	
Phe	Thr	Ile	Ser	Leu	Lys	Glu	Gln	Ser	Lys	Pro	Ser	Met	Gly	Glu	Gln
			500					505					510		
Glu	Leu	Glu	Thr	Tyr	Trp	Lys	Ala	Val	Leu	Asp	Ala	Leu	Gly	Gly	Gly
		515					520					525			
Gly	Gly	Asn	Asn	Lys	Gly	Ala	Glu	Asn	Val	Asn	Gly	Leu	Gly	Glu	Leu
	530					535					540				
Met	Val	Glu	Ile	Leu	Ser	Ala	Asp	Ser	Gly	Leu	Leu	Arg	Gly	Gly	Gly
545					550					555					560
Leu	Gly	Gly	Asp	Ile	Gly	Phe	Glu	Gly	Lys	Met	Lys	Gln	Lys	Arg	Glu
				565					570					575	
Asp	Glu	Glu	Val	Arg	Asn	Met	His	Leu	Val	Asp	Lys	Lys	Gly	Tyr	Val
			580					585					590		
Phe	Glu	Ala	Ala	Lys	Tyr	Val	His	Val	Ser	Lys	Gly	Phe	Ala	Ala	Leu
		595					600					605			
Ser	Phe	Tyr	Leu	Leu	Tyr	Ala	Ala	Ala	Ala	Thr	Ser	Asn	Pro	Ser	Ile
	610														

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226

Lys Lys Ala Lys Gln Asp Leu Ile Arg Asn Ala Ser Ile Gly Arg Leu
 755 760 765
 Ile Val Glu Pro Val Gly Lys Thr Pro Ile Ser Ser Ile Ala Leu Phe
 770 775 780
 Arg Ser Met Lys Arg Ser Arg Ser Glu Asp Leu Lys Met Gly Ser Asn
 785 790 795 800
 Asn Lys Tyr Arg Leu Ala Arg Asp Thr Lys Thr Ala Thr Pro Arg Asn
 805 810 815
 Pro Leu Ser Tyr Thr Gly Lys Ile Val Phe Ser Leu Asp Asp Leu Lys
 820 825 830
 Asn Phe Ser Lys Asp Ser Tyr Thr Thr Met Lys Val Phe Pro Leu Thr
 835 840 845
 Pro Leu Asp Gly
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<210> 142
 <211> 591
 <212> DNA
 <213> SHRIMP

<400> 142
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 aaggagggaa ggtacgtccg atcgttggcc accatggacg aattggaggt acctgaagaa 180
 ccagccactt gctacacttg cggctacacc tttattagac gcagggcacc cccacaaaa 240
 cgcaagtcaa tattcagaga gccttgcgct taccagaac ttctccccga tgcaccatcc 300
 ccggtccgtt tagaagagct gtgcgacgtg ccagaaggag cgagtttttt cacctaccct 360
 ccctacgacg acggatcttc tacatcgtct tcacaagccg aatgtgaaga tgattatcct 420
 ccaccatacg acccatcaga aaatccacag aggtcccaag tgtgtgatta ttgtaccaca 480
 cgtcaagtcc tcagttctat gacggatcac gccagggcca acctcataaa aaatctgaag 540
 agggagaaga aggcctggg tcttggccgt cgcaacaact ttagctacta g 591

<210> 143
 <211> 194
 <212> PRT
 <213> SHRIMP

<400> 143
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 Asp Met Asp Asp Leu Gln Arg Ala Thr Tyr Lys Asp Arg Met Glu Leu
 20 25 30
 Val Leu Glu Met Ala Lys Lys Glu Gly Arg Tyr Val Arg Ser Leu Ala
 35 40 45
 Thr Met Asp Glu Leu Glu Val Pro Glu Glu Pro Ala Thr Cys Tyr Thr
 50 55 60
 Cys Gly Tyr Thr Phe Ile Arg Arg Arg Ala Pro Pro Pro Lys Arg Lys
 65 70 75 80
 Ser Ile Phe Arg Glu Pro Cys Ala Tyr Pro Glu Leu Leu Pro Asp Ala
 85 90 95
 Pro Ser Pro Val Arg Leu Glu Glu Leu Val Asp Val Pro Glu Gly Ala
 100 105 110
 Ser Phe Phe Thr Tyr Pro Pro Tyr Asp Asp Gly Ser Ser Thr Ser Ser
 115 120 125
 Ser Gln Ala Glu Cys Glu Asp Tyr Pro Pro Pro Tyr Asp Pro Ser
 130 135 140
 Glu Asn Pro Gln Arg Ser Gln Val Cys Asp Tyr Cys Thr Thr Arg Gln
 145 150 155 160
 Val Leu Ser Ser Met Thr Asp His Ala Arg Ala Asn Leu Ile Lys Asn
 165 170 175

<213> SHRIMP

<400> 146

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cttcgagacg acactattcc agttctcact accaagaaaa ttttctggag aggagttgtg 180
gaagaactct tgtggttcat caggggcaat acagacgcca aagaattggc caagaagaag 240
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agagcagagg gagatttggg acccgatac ggattccaat ggcgtcattt tggtgctgaa 360
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aagaccctga gagaaaatcc agatgataga aggatgatta tgacggcatg gaatcctatg 480
gatcttcacc ttatggctct tcctccatgc cacatgactg ctcaatttta tgtggctaata 540
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aatattgcat catactctct tctgactcat ctgatggcca gtatgggtgg tctaaaaccg 660
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aagaagcagt tgtgccgcgt ccctagacca ttccctaagt tgaggatttt aatggctcca 780
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ggaaacttgc agatgaaaat ggctgtttga 870

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<210> 147

<211> 285

<212> PRT

<213> SHRIMP

<400> 147

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Met Glu Gly Glu His Gln Tyr Leu Asn Leu Val Arg Glu Ile Arg Gly
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Val Lys Lys Asp Asp Arg Thr Gly Thr Gly Thr Leu Ser Ile Phe Gly
          20          25          30
Pro Gln Met Arg Phe Ser Leu Arg Asp Asp Thr Ile Pro Val Leu Thr
          35          40          45
Thr Lys Lys Ile Phe Trp Arg Gly Val Val Glu Glu Leu Leu Trp Phe
          50          55          60
Ile Arg Gly Asn Thr Asp Ala Lys Glu Leu Ala Lys Lys Lys Ile His
          65          70          75          80
Ile Trp Asn Ala Asn Gly Ser Arg Glu Phe Leu Asp Ser Arg Gly Asp
          85          90          95
Arg Ala Glu Gly Asp Leu Gly Pro Val Tyr Gly Phe Gln Trp Arg His
          100          105          110
Phe Gly Ala Glu Tyr Asp Thr Cys Ser Ser Asp Tyr Thr Gly Lys Gly
          115          120          125
Ile Asp Gln Leu Ala Asn Ile Leu Lys Thr Leu Arg Glu Asn Pro Asp
          130          135          140
Asp Arg Arg Met Ile Met Thr Ala Trp Asn Pro Met Asp Leu His Leu
          145          150          155          160
Met Ala Leu Pro Pro Cys His Met Thr Ala Gln Phe Tyr Val Ala Asn
          165          170          175          180
Gly Glu Leu Ser Cys Gln Leu Tyr Gln Arg Ser Gly Asp Val Gly Leu
          180          185          190
Gly Val Pro Phe Asn Ile Ala Ser Tyr Ser Leu Leu Thr His Leu Met
          195          200          205
Ala Ser Met Val Gly Leu Lys Pro Gly Glu Phe Ile Leu Thr Leu Gly
          210          215          220
Asp Ala His Ile Tyr Asn Thr His Ile Glu Val Leu Lys Lys Gln Leu
          225          230          235          240
Cys Arg Val Pro Arg Pro Phe Pro Lys Leu Arg Ile Leu Met Ala Pro
          245          250          255
Glu Lys Ile Glu Asp Phe Thr Ile Asp Met Phe Tyr Leu Glu Gly Tyr
          260          265          270
Gln Pro His Ser Gly Asn Leu Gln Met Lys Met Ala Val
          275          280          285

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229

<210> 148
 <211> 678
 <212> DNA
 <213> SHRIMP

<400> 148
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 ggtattgagg tgatgaagag gcgtctcgta cggcaaggaa agtgtgggaa ttttgaagca 180
 agtggaggtg ctatgtcgta tttctggctc gaagataatg cagaagatat ggagaatctc 240
 aacagtgggt cccatgtcaa gacaaactgc ttggcattat tccttcaaga gtttatcagc 300
 aactggattg aagagactga tcgacatgga cagtactgta cttttcccca atacatggac 360
 ggtggggatg gttcacgtgg gggatatttt acttcgctag ccatgaaatg gatggctagg 420
 gatgtgactt tctttgtgtt tgttgatagg aataatactg tagaaaatgc ggcatccata 480
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 gcatcaaacc caatgttttc tgtatgtaat gcgtgtagg gcaagtaccc aggcccagtg 600
 tcatacgtta ttgaaggcca tggagtgggt cattctgatt tgacatgtga tgagatttct 660
 ggattctttg tataataa 678

<210> 149
 <211> 220
 <212> PRT
 <213> SHRIMP

<400> 149
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 Asp Asn Asn Pro Met Phe Ser Val Cys Asn Ala Cys Arg Cys Lys Tyr
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<212> PRT

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Lys Asn Gln Leu Glu Asn Phe Asp Tyr Glu Asp Met Thr Arg Leu Ile
180    185    190
Phe Asp Asn Ile Pro Glu Thr Asp Tyr Leu Trp Thr Thr His Phe Asp
195    200    205
Pro Lys Lys Tyr Asp Thr Tyr Ser Glu Lys Val Leu Gly Phe Ser Asp
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Thr Gln

<213> SHRIMP

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<213> SHRIMP

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His Asp Phe Gly Lys Ile Ser Thr Gly Asp Gly Gly Thr Phe His Leu
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Phe Glu Asp Thr Pro Gly Phe Glu Ser Ala Leu Lys Ala Glu Tyr Lys
115 120 125
Asn Val Pro Gly Ala Thr Thr Pro Lys Tyr Val Ser Met Asn Ser Leu
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Arg Ile Asp Ala Ile Asn Gly Lys Ile Glu Glu Val Tyr Asn Pro Ser
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Pro Ile Met Gly Ile Arg Glu Tyr Gly Thr Ile Arg Arg Gly Arg Tyr
165 170 175
Glu Glu Asn Ala Gly Ser Lys Glu Leu Val Phe Met Thr Lys Ile Glu
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Lys Arg Pro Asn Asn Val Ala Glu Asn Leu Ile Ile Arg Val Ala Asn
195 200 205
Gln Gln Tyr Asn Val Met Arg Met Val Phe Phe Ile Asp Tyr Glu Thr
210 215 220
Lys Lys Gly Val Ser Lys Glu Glu Met Phe Ile Pro Tyr Asn Val Gln
225 230 235 240
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35 40 45
Leu Glu Leu Ile Gly Val Leu Ser Gly Val Ser Asp Asn Val Val Thr
50 55 60
Gln Ile Ser Pro Asp Gln Ile Phe Val Gly Thr Tyr Met Val Lys Tyr

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			100						105					110		
	Thr	Ser	Ser	Asp	Phe	Lys	Met	Lys	Tyr	Thr	Arg	Ser	Leu	Met	Asp	His
		115						120					125			
	Thr	Glu	Lys	Tyr	Tyr	Phe	Ser	Gly	Asp	Gln	Lys	Leu	Ser	Lys	Ile	Ser
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 35 40 45
 Ile Arg Gln Ile Val Asp Lys Ile Arg Ser Gln Thr Thr Ser Asp Ile
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 115 120 125
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 130 135 140
 Cys Gly Ile Ile Arg Tyr Thr Val Phe Val Asn Asn Leu Ala Arg Ser
 145 150 155 160

Thr Leu Asp Asn Asp Asp Asp Lys Ala Ala Thr Tyr Tyr Asn Thr Pro
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 Asp Ser Tyr Ser Lys Val Glu Ala Glu His Thr Val Glu Gly Arg Lys
 195 200 205
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 Thr Ile Ile Pro Ser Val Thr Gly Tyr Leu Ala Ser Ile Ser Glu Asp
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 Ala Asp Val Gln Ala Pro Leu Leu Leu Asn Cys Asn Asn Cys Phe Ile
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 <213> SHRIMP

<400> 159

Met	Gln	Leu	Arg	Leu	Glu	Asn	Phe	Val	Lys	Glu	Glu	His	Glu	Thr	Val	1	5	10	15
Val	Val	His	Asn	Pro	Ser	Gly	Met	Thr	Gly	Phe	Asn	Ile	Phe	Asn	Ser	20	25	30	
Ser	Pro	Val	Tyr	Phe	Glu	Val	His	Asn	Glu	Met	Asp	Ala	Leu	Ile	Phe	35	40	45	
Met	Ala	Ala	Phe	Leu	Lys	His	Asn	Ser	Leu	Trp	Gly	Glu	Ile	Asn	Ala	50	55	60	
Asn	Met	Asp	Leu	Tyr	Thr	Phe	Asp	Tyr	Ala	Gly	Ala	Phe	Leu	Asp	Glu	65	70	75	80
Arg	Trp	Cys	His	His	Glu	Lys	Ser	Phe	Ser	Val	Val	Arg	Ala	Gln	Leu	85	90	95	
Ile	Asn	Ser	Tyr	Tyr	Lys	Cys	Arg	Arg	Lys	Ile	Met	Gln	Ala	Leu	Asp	100	105	110	
Asn	Asn	Tyr	Asn	Asn	Lys	Asn	Lys	Lys	Arg	Lys	Asn	Val	Gly	Gly	Ala	115	120	125	
Pro	Ala	Phe	Thr	Phe	Met	Ser	Gly	Asp	Gly	Glu	Gly	Gly	Lys	Glu	Ala	130	135	140	
Leu	Glu	Ala	Ser	Phe	Asp	Val	Ile	Gly	Gly	Thr	Arg	Gly	Gly	Arg	Phe	145	150	155	160
Gly	Val	Asp	Ser	Thr	Pro	Cys	Pro	His	Ser	Ser	Ala	Met	Gln	Leu	Lys	165	170	175	
Leu	Asp	Asn	Glu	Gly	Asn	Tyr	Gly	Cys	Ile	Ala	Cys	Phe	Ala	Ser	Met	180	185	190	
Phe	Phe	Val	Leu	Glu	Asn	Pro	Gly	Asp	Glu	Ser	Ser	Phe	Ile	Ser	Thr	195	200	205	
Asp	Ala	Ser	Lys	Ile	Gly	Gln	Ala	Gln	Ala	Trp	Ile	Asp	Glu	Arg	Leu	210	215	220	
Arg	Asn	Asn	Glu	Asn	Gly	Gly	Glu	Glu	Asn	Asn	Val	Phe	Lys	Lys	Thr	225	230	235	240
Phe	His	Met	Leu	Ala	Asp	Ile	Thr	Gln	Lys	Ala	His	Glu	Thr	Ala	Tyr	245	250	255	
Ser	Asn	Thr	Ile	Pro	Leu	Gly	Pro	Asn	Gly	Arg	Gln	Trp	Asn	Trp	Pro	260	265	270	
Thr	His	Thr	Val	Glu	Pro	Ile	Ala	His	Glu	Phe	Val	Thr	His	Ser	Leu	275	280	285	
Val	Asn	Thr	Leu	Lys	Asn	Leu	Gly	Asp	Arg	Lys	Leu	Pro	Arg	Phe	Asn	290	295	300	
Phe	Asp	Ile	Leu	Tyr	Asn	Leu	Leu	Asn	Pro	Phe	Gly	Lys	Met	Leu	Leu	305	310	315	320

Val	Phe	Ile	Gln	Asn	Cys	His	Ile	Leu	Thr	Gly	His	Lys	Asn	Asn	Glu
				325					330					335	
Asn	Val	Val	Pro	Arg	Gly	Ser	Ala	Ser	Gly	Lys	Trp	Trp	Thr	Ile	Asn
			340					345						350	
Phe	Val	Gly	Val	Asn	Met	Trp	Thr	Phe	Gln	Val	Thr	Lys	Cys	Lys	Val
		355					360					365			
Glu	Lys	Asp	Arg	Lys	Ile	Ser	Asp	Leu	Ala	Cys	Met	Leu	Pro	Arg	Leu
		370					375				380				
Pro	Asn	Pro	Gly	Ser	Thr	Thr	Val	Asp	Asp	Arg	Ile	Val	Phe	Lys	Gly
385						390				395					400
Phe	Cys	Arg	Gly	Glu	Asn	Leu	Gly	Ser	Val	Gly	Glu	Val	Val	Ser	Asp
				405					410					415	
Ile	Thr	Gln	Ser	Val	Lys	Asn	Phe	Cys	Leu	Met	Val	Glu	Asn	Arg	Lys
			420					425						430	
Phe	Ser	Val	Asp	Lys	Glu	Thr	Gly	Phe	Ile	Ser	Ser	Glu	Ser	Ile	Val
		435					440					445			
Ser	Asp	Pro	Phe	Phe	Ser	Leu	Glu	Val	Thr	Gly	Cys	Arg	Ser	Asn	Arg
		450				455					460				
Ala	Gln	Asp	Thr	Ile	Asn	Asn	Gly	Arg	Val	Ser	Ala	Arg	Val	Met	Arg
465						470				475					480
Ile	Leu	Lys	Ser	Arg	Glu	Gly	Ala	Arg	Val	Trp	Leu	Ala	Lys	Asp	Glu
				485					490					495	
Asn	Ala	Ile	Ile	Phe	Glu	Asn	Val	Asn	His	Asp	Thr	Ala	Ile	Ser	Thr
			500					505					510		
Asp	Ala	Met	Glu	Arg	Ala	Ile	Gly	Gln	His	Lys	Ile	Leu	Tyr	Tyr	Asp
		515					520					525			
Ile	Glu	Thr	Thr	Asp	Lys	Asp	Phe	Thr	Asp	Lys	Lys	Ser	Val	Ile	Thr
		530				535					540				
Ser	Ile	Gly	Phe	Cys	Leu	Cys	Thr	Gly	Gly	Asp	Met	Thr	His	Gly	Gly
545					550					555					560
Glu	Arg	Gly	Val	Phe	Gly	Leu	Val	Ala	Pro	Gly	Ser	Asp	Val	Glu	Lys
				565					570					575	
Val	Lys	Glu	Thr	Ile	Ile	Asn	Ser	Tyr	Asp	Pro	Glu	Glu	Lys	Glu	Asp
			580					585					590		
Ile	Met	Lys	Gln	Cys	Pro	Gln	Val	Ile	Glu	Ile	Phe	Thr	Asn	Glu	Phe
		595					600					605			
Glu	Met	Leu	Leu	Gly	Phe	Gly	Lys	Tyr	Ile	Asp	Lys	Val	Lys	Pro	His
		610					615					620			
Val	Ile	Ser	Gly	Trp	Asn	Asn	Val	Ala	Phe	Asp	Asp	Pro	Phe	Val	Phe
625					630					635					640
Thr	Arg	Ile	Val	Lys	His	Leu	Ser	Asp	His	Thr	Lys	Asp	Met	Ser	Tyr
				645					650					655	
Cys	Val	Ala	Asp	Ala	Ser	Thr	Ala	Glu	Ser	Val	Leu	Pro	Arg	Ala	Thr
			660					665					670		
Glu	Gly	Gly	Gly	Gly	Gly	Glu	Thr	Pro	Tyr	Arg	Leu	Ser	Thr	Pro	Gln
		675					680					685			
Glu	Arg	Ile	Gln	Leu	Ala	Ser	Thr	Gly	Ile	Phe	Asn	Lys	Leu	Gly	Lys
		690				695					700				
Phe	Val	Asp	Lys	Lys	Thr	Gly	Met	Leu	Lys	Pro	Glu	Met	Thr	Ala	Asp
705					710					715					720
Leu	Leu	Ala	Gly	Ala	Glu	Ser	Gln	Ala	Asn	Thr	Lys	Phe	Lys	Glu	Arg
				725					730					735	
Asn	Lys	Leu	Ser	Ser	Ser	Asn	Lys	Gly	Ser	Ala	Gly	Trp	Phe	Gln	Lys
			740					745					750		
Ile	Ile	Gly	Gly	Met	Cys	Ser	Ala	Ile	Arg	Leu	Asp	Leu	Met	Lys	Val
		755					760					765			
Cys	Glu	Lys	Ala	Tyr	Lys	Glu	Ser	Leu	Ser	Glu	Phe	Asn	Leu	Asn	Ala
		770				775					780				
Val	Leu	Ala	Lys	Val	Ser	Ser	Val	Gly	Asp	Lys	Val	Lys	Asn	Val	Lys
785					790					795					800
Asp	Glu	Val	Asp	Leu	His	Phe	His	Leu	Leu	Gly	Phe	Leu	Lys	Leu	Lys

				805					810					815	
Lys	Ala	Gln	Asp	Gln	Ala	Lys	Val	His	Val	Tyr	Cys	Cys	Lys	Asp	Ala
			820					825					830		
Tyr	Leu	Thr	Gly	Ile	Val	Ser	Thr	Ser	Ile	Asn	Lys	Glu	Gly	Glu	Ile
		835					840					845			
Phe	Arg	Leu	Cys	Met	Asp	Ser	Ala	Leu	Thr	Glu	Ala	Val	Val	Thr	Ala
	850						855					860			
Asn	Leu	Ala	Thr	Pro	Leu	Cys	Ile	Gly	Glu	Gly	Ala	Ile	Cys	Arg	Asn
865					870					875					880
Met	Gly	Glu	Glu	Arg	Ala	Asp	Arg	Arg	Gly	Val	Gly	Val	Arg	Arg	His
				885					890					895	
Ser	Ile	Ala	Thr	Asp	Thr	Lys	Gly	Gly	Met	Val	Ser	Gln	Pro	Ile	Val
			900					905					910		
Asn	His	Val	Pro	Tyr	Gln	Thr	Ile	Asp	Met	Thr	Ser	Leu	Tyr	Pro	Met
	915						920					925			
Thr	Met	Cys	Gln	Asn	Asn	Leu	Cys	Thr	Thr	Thr	Phe	Val	Thr	Gln	Ile
	930					935					940				
Met	Gln	Leu	Arg	Asp	Arg	Leu	Val	Leu	Glu	Lys	Met	Lys	Asn	Lys	Thr
945					950					955					960
Thr	Asp	Ser	Leu	Leu	Leu	Leu	Asp	Val	Ile	Asp	Glu	Cys	Asn	Gln	Ile
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Val	Leu	Ser	Glu	Tyr	Arg	Pro	Ile	Asp	Ile	Ala	Val	Ala	Ser	Trp	Lys
		980						985					990		
Asn	Ser	Asn	Ser	Asn	Arg	Gln	Thr	Pro	Ile	Thr	Arg	Ile	Glu	Glu	Ser
	995					1000						1005			
Leu	Gly	Leu	Arg	Phe	Ile	Glu	Asn	Leu	Asp	Ala	Glu	Lys	Thr	Asn	Asn
	1010					1015					1020				
Lys	Thr	Trp	Cys	Thr	Asn	Thr	Ser	Pro	Asn	Met	Asn	Val	Thr	Ala	Ala
1025					1030					1035					1040
Gly	Met	Asp	Tyr	Phe	Pro	Glu	Ile	Val	Cys	Asp	Ile	Asn	Met	Gln	Phe
				1045					1050					1055	
Ala	Ala	Lys	Val	Asn	Asp	Asp	Met	His	Ile	Ala	Pro	Ala	Ser	Leu	Glu
		1060						1065					1070		
Tyr	Met	Leu	Gln	Val	Leu	Pro	Ile	Met	Leu	Ile	Asp	Arg	Pro	Tyr	Ile
	1075						1080					1085			
Gly	Ala	His	Ile	Thr	Ala	Gly	Lys	Cys	Arg	Thr	Leu	Glu	Asp	Ile	Leu
	1090					1095					1100				
Ser	Glu	Leu	Glu	Lys	Asp	Phe	Ser	Val	Glu	Lys	Asp	Glu	Glu	Ile	Ile
1105					1110					1115					1120
Arg	Thr	His	Trp	Thr	Phe	Lys	Gly	Gln	Lys	Gln	Tyr	Asp	Phe	Cys	His
				1125					1130					1135	
Ser	Pro	Val	Thr	Gln	Met	Ala	Arg	His	Ile	Ile	Glu	Ser	Thr	Gly	Arg
		1140						1145					1150		
Asn	Ile	Arg	Asp	Tyr	Glu	Gly	Asn	Glu	Lys	Phe	Glu	Arg	Leu	Val	Ser
	1155						1160					1165			
Leu	Ser	Asp	Arg	Ile	Tyr	Arg	Arg	Val	Gly	Ala	Phe	Asp	Ser	Ala	Asn
	1170					1175					1180				
Asp	Pro	Ala	Val	Arg	Leu	Trp	Ser	Ser	Arg	Leu	Ile	Asn	Val	Gly	Met
1185					1190					1195					1200
Leu	Val	Arg	Thr	Trp	Asn	Val	Lys	Thr	Asp	Ile	Leu	Lys	Gly	Ile	Ile
			1205						1210					1215	
Pro	Gln	Met	Gln	Ala	Tyr	Ala	Asp	Arg	Val	Val	Met	Gln	Asn	Lys	Ala
		1220						1225					1230		
Lys	Glu	Phe	Ala	Lys	Met	Gly	Asp	Met	Lys	Arg	Ala	Gln	Lys	Val	Gly
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Gln	Asn	Ile	Met	Lys	Leu	Gly	Met	Asn	Ser	Met	Tyr	Gly	His	Leu	Ala
	1250					1255					1260				
Leu	Arg	Ala	Arg	Ser	Ser	Arg	Lys	Glu	Phe	Ala	Ser	Gly	Ser	Ala	Asn
1265					1270					1275					1280
Thr	Ala	Ser	Ser	Ile	Ser	Asn	Met	Ser	Ala	Thr	Gly	Gly	Ile	Gly	Gly
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Gly Thr Arg His Ser Val Thr Ala Asn Gln Ile Thr Glu Asn Ala Arg
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 Cys Val Phe Gly Asn Ile Gly Cys Gly Leu Gln Met Ala Leu Pro Gly
 1315 1320 1325
 Thr Lys Gln Thr Tyr Gly Asp Thr Asp Ser Val Phe Cys Val His Asn
 1330 1335 1340
 Ile Val Gly Asp Gly Gly Met Ile Pro Glu Tyr Asp Glu Gln Thr Gly
 1345 1350 1355 1360
 Lys Tyr Tyr Tyr Val Met Asp Ile Ala Leu Lys Asn Lys Met Ala Ala
 1365 1370 1375
 Ile Ile Pro Ile Leu Val Asn Ser Leu Thr Lys Gly Ile Gln Phe Val
 1380 1385 1390
 Glu Arg Arg Asp Ala Gly Val Gly Met Met Asn Ile Ala His Glu Arg
 1395 1400 1405
 Leu Ala Val Ala Gly Leu Leu Phe Ala Lys Lys Thr Tyr His Met Leu
 1410 1415 1420
 His Phe Asn Glu Asn Ser Ala Ala Phe Asn Asp Met Ile Lys Leu Lys
 1425 1430 1435 1440
 Ser Thr Asp Asn Asn Asn Lys Phe Ala Ser Phe Ile Lys Arg Pro Ser
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 His Ala Asp Gly Tyr Val Val Pro His Asn Pro Ser Leu Ile Leu Arg
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 Ala Ala Glu Gly Pro Ala Gly Lys Lys Leu Lys Ser Phe Leu Glu Glu
 1475 1480 1485
 Glu Gly Ile His Asp Glu Lys Ser Met Glu Glu Trp Phe Thr Ser Ser
 1490 1495 1500
 Pro Thr Trp Met Ala Met Asp Ala Ser Val Ile Asn Asn Leu Tyr Ala
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 Ser Gln Ile Val Gly Val Glu Lys Gly Asn Trp Ile Asp Ala Met Thr
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 Ser Arg Pro Ile Glu Ala Gly Thr Glu Met Met Glu Ala Val Thr Gln
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 Ala Asn Ala Ala Phe Thr Pro Tyr Lys Lys Gly Ala Phe Val Lys Lys
 1555 1560 1565
 Gly Ile Thr Pro Thr Thr Lys Leu Lys Gly Leu Gln Ser Leu Ile Ala
 1570 1575 1580
 Arg Phe Leu Pro Lys Ile Glu Glu Lys Lys Ser Cys Tyr Leu Asp Val
 1585 1590 1595 1600
 Met Lys Asn His Val Glu Asn Phe Ala Ser His Ile Thr Asn Pro Ala
 1605 1610 1615
 Met Met Ile Thr Ser Ser Arg Val Asn Lys Phe Asp Thr Ser Lys Glu
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 Gln Ser Arg Pro Asn Pro Leu Ala Ile Asn Asn His Leu Asn Pro Ser
 1635 1640 1645
 Ser Glu Ile Ser Leu Gly Gln Lys Phe Lys Thr Val Thr Ser Val Ser
 1650 1655 1660
 Ser Trp Ser Leu Ser Ala Glu Glu Gly Glu Val Pro Ala Gly Tyr Phe
 1665 1670 1675 1680
 Asn Ala Gly Ser Val Arg Trp Asp Ala Thr Asn Met Lys Gly Ser Val
 1685 1690 1695
 Pro Ala Phe Ser Val Lys Asn Leu Ser Val Val Pro Asn Ala Ile Thr
 1700 1705 1710
 Ser Val Tyr Lys Met Val Glu Ser Asp Lys Thr Ala Ile Lys Ser Met
 1715 1720 1725
 Ile Ala Lys Asn Val Glu Val Leu Cys Ser Thr Ser Ala Asn Thr Gly
 1730 1735 1740
 Phe Ser Leu Arg Arg Gly Ala Leu Ser Phe Asn Thr Gly Val Ile Val
 1745 1750 1755 1760
 Thr Lys Asp Val Ala Met Ala Cys Ile Arg Ser Leu Asn Asn Lys Gln
 1765 1770 1775
 Met Leu Leu Phe Val Gly Gly Gly Lys Asp Tyr Gly Glu Asp Asp Asp

1780										1785					1790					
Asp	Asp	Asp	Glu	Glu	Ala	Glu	Glu	Glu	Asp	Glu	Glu	Asn	Gly	Glu	Asn					
1795										1800					1805					
Glu	Glu	Asn	Lys	Gly	Asp	Cys	Val	Thr	Glu	Lys	Lys	Ile	Pro	Gly	Arg					
1810										1815					1820					
Ser	Thr	Asn	Lys	Asp	Val	Gly	Glu	Glu	Thr	Lys	Thr	Ser	Glu	Lys	Thr					
1825										1830					1835					
Glu	Gly	Glu	Arg	Lys	Gly	Ser	Lys	Thr	Ala	Lys	Gly	Lys	Thr	Glu	Glu					
1845										1850					1855					
Ile	Ala	Ser	Ser	Leu	Ser	Lys	Cys	Gly	Lys	Lys	Asp	Ala	Arg	Asp	Val					
1860										1865					1870					
Ile	Leu	Asp	Arg	Leu	Leu	Lys	Ala	Thr	His	Ser	Ser	Cys	Thr	Asn	Asn					
1875										1880					1885					
Glu	Glu	Arg	Thr	Arg	Val	Leu	Gln	Gln	Tyr	Ser	Asn	Cys	Thr	Leu	Ser					
1890										1895					1900					
Ser	Tyr	Ile	Thr	Ser	Val	Met	Lys	Leu	Asp	Gln	Arg	Val	Ala	Asp	Gln					
1905										1910					1915					
Met	Glu	Asn	Leu	Ile	Ser	Gln	Leu	Asp	Gln	Ile	Arg	Asn	Leu	Ser	Asn					
1925										1930					1935					
Lys	Lys	Arg	Gln	Glu	Lys	Gly	Gly	Pro	Phe	Lys	Ser	Glu	Leu	Asp	Ala					
1940										1945					1950					
Met	Val	Ala	Ala	Val	Lys	Val	Lys	Phe	Phe	Pro	Val	Leu	Asp	Ala	Ser					
1955										1960					1965					
Arg	Lys	Leu	Thr	Gln	Asp	His	Trp	Lys	Lys	Cys	Pro	Val	Ser	Ile	Pro					
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Glu	Thr	Arg	Glu	Glu	Lys	Pro	Leu	Met	Gly	Val	Pro	Phe	Glu	Val	Asn					
1985										1990					1995					
Ser	Leu	Ile	Gly	Lys	His	Lys	Cys	Thr	Asp	Thr	Cys	Asp	Met	Ala	Cys					
2005										2010					2015					
Cys	Gln	Ser	Leu	Tyr	Phe	Val	Leu	Leu	Tyr	Thr	Leu	Ala	Leu	Lys	Phe					
2020										2025					2030					
Glu	Asn	Glu	Arg	Leu	Ala	Arg	Gln	Ile	Gly	Leu	Asp	Asp	Ser	Val	Asp					
2035										2040					2045					
Leu	Met	Ala	Glu	Met	Leu	Phe	Gly	Gly	Asp	Lys	Leu	Leu	Ala	Gln	Glu					
2050										2055					2060					
Val	Leu	Lys	Arg	Val	Lys	Asp	Ala	Gln	Asp	Arg	Lys	Leu	Val	Lys	Ser					
2065										2070					2075					
Leu	Leu	Pro	Leu	Asn	Tyr	Asn	His	Asp	Thr	Asn	Thr	Ile	Ile	Phe	Leu					
2085										2090					2095					
Phe	Glu	Ser	Leu	Arg	Phe	Ala	Gln	Lys	Pro	Val	Ala	Gly	Met	Ser	Val					
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Ser	Glu	Ile	Lys	Asp	Ala	Val	Arg	Gly	Leu	Ala	Phe	Ser	Thr	Thr	Thr					
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Gly	Thr	Val	Trp	Asn	Tyr	Thr	Asp	Glu	Arg	Phe	Phe	Gly	Pro	Leu	Tyr					
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Asn	Met	Asp	Glu	Leu	Cys	Asn	Glu	Arg	Val	Asn	Gly	Asn	Cys	Lys	Leu					
2145										2150					2155					
Ser	Phe	Ile	Thr	Gly	Ile	Tyr	His	Thr	Ala	Ala	Val	Glu	Leu	Ala	Ala					
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<212> PRT

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<220>

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<400> 161

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Pro Gln Gly Glu Arg Gly Ala Ile Gly Pro Ala Gly Lys Asp Gly Ala
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Gly Arg Asp Gly Ala Val Gly Pro Ala Gly Pro Pro Gly Glu Arg Gly
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Ala Ile Gly Pro Ala Gly Arg Asp Gly Ala Val Gly Pro Ala Gly Pro
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Pro Gly Glu Arg Gly Ala Thr Gly Ile Pro Gly Arg Asp Gly Val Asp
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Gly Pro Pro Gly Lys Asp Gly Val Asp Gly Ser Glu Gly Pro Gln Gly
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Ile	Gly	Pro	Ile	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Glu	Thr	Gly	Arg	Pro
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Cys Arg Thr Asp Val Ser Thr Asn Ala Arg Ser Val Asn Ala Val Arg		
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WO 01/38351

PCT/US00/28888

245

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<212> DNA

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Thr	Ser	Ser	Thr 660	Thr	Pro	Asp	Met	Val 665	Ser	Ser	Leu	Glu	Glu 670	Gly	Ala
Thr	Ser	Thr 675	Ser	Ser	Ser	Asp	Glu 680	Asn	Gln	Ile	Ala	Ser 685	Leu	Glu	Asn
Ile	Lys 690	Lys	Leu	Leu	Ser	Ile 695	Ile	Thr	Ser	Thr	Phe 700	Ala	Thr	Gly	Ala
Asp 705	Lys	Asn	Asp	Thr	Ile 710	Phe	Ala	Trp	Thr	Val 715	Val	Thr	Leu	Ala	Glu 720
Arg	Phe	Cys	Ala	Leu 725	Tyr	Asn	Ile	Thr	Ser 730	His	Pro	Glu	Glu 735	Tyr	Tyr
Gln	Gln	Ile	Ile 740	Arg	Glu	Asp	Phe	Glu 745	Phe	Glu	Gly	Gly	Phe 750	Glu	Lys
Phe	Arg	His 755	Met	Cys	Asp	Ala	Ile 760	Asn	Arg	Glu	Leu	Ser 765	Ile	Tyr	Val
Pro	Lys 770	Ser	Val	Leu	Glu	Lys 775	Gln	Ser	Val	Cys 780	Arg	Met	Gly	Val	Ala
Ala 785	Tyr	Glu	Asn	Ser	Met 790	Glu	Arg	Ile	Lys	Asn 795	Lys	Thr	Asn	Ser	Lys 800
Leu	Cys	Lys	Ile	Lys 805	Tyr	Asp	Glu	Ser	Thr 810	Met	Val	Tyr	Glu 815	Leu	Asn
Asn	Asp	Thr	Phe 820	Lys	Thr	Phe	Asp	Tyr 825	Asp	Glu	Ser	Asp	Lys 830	Ser	Phe
Gly	Pro	Met 835	Tyr	Glu	Cys	Ala	Pro 840	Met	Phe	Gln	Arg	Leu 845	Phe	Ala	Ser
Val	Lys 850	Ser	Asp	Lys	Glu	Ala 855	Val	Leu	Ala	Asp	Lys 860	Lys	Ser	Glu	Lys
Arg 865	Glu	Lys	Leu	Tyr	Gln 870	Gln	Lys	Gln	Glu	Tyr 875	Leu	Arg	Lys	Cys	Asp 880
Asn	Asp	Asp	Val	Ser 885	Ala	Arg	Gln	Ile	Leu 890	Asn	Asn	Val	Asn	Glu	Ser
Asp	Glu	Glu	Ser	Asp	Glu	Glu	Ser	Asp	Asp	Glu	Glu	Asn	Tyr	Gly	Ala

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Ala	Lys	Gly	Gly	Ala	Thr	Gly	Asp	Tyr	Tyr	Gly	Gly	Asp	Asp	Glu	Asp	
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Asp	Cys	Tyr	Gly	Phe	Leu	Gly	Glu	Phe	Gly	Ser	Ser	Asp	Asp	Glu	Asn	
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Val	Pro	Ser	Asp	Asn	Ala	Ser	Ser	Ile	Asn	Asn	Val	Gln	Asp	Asp	Val	
945					950					955					960	
Phe	Arg	Asp	Val	Asn	Phe	Ile	Lys	Thr	Phe	Asn	Phe	Arg	Ser	Ser	Leu	
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Cys	His	Arg	Gln	Lys	Tyr	Val	Ser	Thr	Val	Ile	Val	Glu	Glu	Met	Glu	
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Lys	Asn	Leu	Cys	Asp	Val	Leu	Thr	Leu	Asp	Asn	Ser	Ala	Ala	Glu	Ser	
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Gly	Asp	Ile	Leu	Lys	Glu	Ile	Asn	Arg	Arg	Ser	Leu	Arg	Met	Arg	Asn	
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Trp	Val	Val	Pro	Phe	Thr	Met	Pro	Val	Arg	Glu	Ile	Val	Lys	Pro	Asn	
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Val	Asn	Ser	Glu	Asp	Gly	Thr	Ala	Asn	Ser	Asn	Asn	Asn	Ile	Pro	Pro	
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Phe	Cys	Ser	Cys	Ala	Ser	Leu	Asn	Asn	Phe	Lys	Ser	Asp	Ser	Pro	Leu	
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Ser	Ser	Asn	Asn	Thr	Met	Ser	Asn	Glu	Lys	Cys	Ile	Lys	Leu	Leu	Pro	
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	1090					1095					1100					
Met	Ala	Cys	Glu	Arg	Arg	Tyr	Phe	Ser	Asp	Val	Thr	Ala	Ala	Leu	Gly	
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Phe	Val	Lys	Lys	Asp	Lys	Val	Asn	Gly	Asn	Ile	Arg	Ser	Ile	Leu	Asp	
				1125					1130					1135		
Asn	Lys	Arg	Trp	Asp	Ala	Ile	Lys	Gln	Cys	Lys	Leu	Ala	Gly	Lys	Cys	
			1140					1145					1150			
Leu	Ser	Ser	Ala	Leu	Pro	Leu	Gly	Ile	Tyr	Glu	Asn	Val	Ile	Ser	Glu	
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Asp	Asn	Lys	Leu	Ile	Asn	Thr	Phe	Arg	Pro	Arg	Ser	Leu	Ala	Arg	Leu	
	1170				1175						1180					
Ala	Cys	Ser	Ser	Gly	Gly	Asp	Gly	Val	Ser	Asp	Lys	Ser	Val	Asn	Asn	
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Gly	Phe	Phe	Ser	Gly	Ile	Trp	Ala	Leu	Cys	Ala	Asn	Gln	Asp	Leu	Glu	
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Ser	Val	Val	Leu	Gly	Ser	Thr	Val	Val	Asp	Pro	Leu	Lys	Pro	Thr	Lys	
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Val	Phe	Asn	Gln	Ser	Leu	Ser	Glu	Lys	Glu	Leu	Lys	Glu				

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 Asn Leu Leu Thr Asn Asn Asn Val Ile Lys Lys Leu Lys Ile Lys Pro
 1425 1430 1435 1440
 Thr Pro Ser Asn Asp Val Arg His Gln Ile Trp Val Glu Asp Glu Tyr
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 Tyr Pro Arg Asn Lys Ser Thr Leu Arg Ser Arg Ala Glu Trp Met Ala
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 Ala Thr Glu Glu Val Leu Lys Thr Glu Met Ser Leu Ser Cys Val Leu
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 Ala Met Val Ala Met Tyr Arg Ile Met Met Gln Gly Glu Ser Val Arg
 1490 1495 1500
 Glu Ile Ala Thr Ala Pro Leu Arg Leu Ser Val Asp Lys Met Val Pro
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 Leu Ile Arg Cys Phe Lys Ile Thr Ser Lys Trp Cys Ser Cys Thr Gly
 1525 1530 1535
 Lys Gly Asp Ser Pro Lys Lys Ala Asp Ala Ser Ile Lys Glu Gly Arg
 1540 1545 1550
 Phe Tyr Asp Ile Glu Glu Asp Pro Leu His Phe Tyr Arg Phe Ala Ala
 1555 1560 1565
 Tyr Val Ile Gly Gln Val Asn Asp Ile Val Ile Glu Glu Met Thr Arg
 1570 1575 1580
 Lys Ile Leu Met Ser Phe Asp Phe Asn Gly Phe Asp Thr Ser Asn Trp
 1585 1590 1595 1600
 Leu Gln Phe Ile Tyr Phe Ser His Val Leu Met Gly Arg Arg Ser Arg
 1605 1610 1615
 Leu Leu Ser Arg Pro Leu Ser Leu Val Lys Asn Leu Val Ser Val Ser
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 Ser Leu Ala Asp Lys Asn Ser Glu Lys Ser Asn Asp Met Tyr Glu Lys
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 Arg Val Gly Lys Val Met Lys Arg Ile Ala Arg Leu Val Leu Val Lys
 1650 1655 1660
 Ala Ala Asp Ser Val Arg Ala Ser Ser Asn Asp Leu Leu Asp Cys Cys
 1665 1670 1675 1680
 Ile Leu Asp Val Asn Asp Val Ser Val Lys Ser Leu Asp Glu Phe Arg
 1685 1690 1695
 Ala Lys Thr Arg Gln Glu Leu Gln Glu Thr Arg Ile Asp Thr Asn Tyr
 1700 1705 1710
 Asn Leu Val Ser Asn Ser Cys Thr Thr Ala Gln Leu Ala Ala Val Glu
 1715 1720 1725
 Lys Ser Ser Arg Ile Ile Asn Thr Asn Ile Ser Phe His Asn Ile Pro
 1730 1735 1740
 Ala Gly Gln Ala Lys Val Met Asp Ala Asn Glu Glu Ala Phe Ile Asp
 1745 1750 1755 1760
 Pro Ser Leu Glu Glu Ile Asn Lys Glu Asp Asn Ser Gly Ala Lys Gln
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 Met Thr Gly Lys Gly Gly Ser Asn Arg Gly Arg Ser Lys Lys Ser Gly
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 Gly Gly Gly Phe Asn Asn Ala Gly Gly Phe Tyr Asn Asp Asp Ser Ser
 1795 1800 1805
 Arg Gly Ser Ser Ser Val Val Asp Glu Asp Ser Arg Ser Arg Thr Gly
 1810 1815 1820
 Phe Ser Gln Ile His Met Asp Ala Arg Asn Glu Glu Asp Arg Glu Ser
 1825 1830 1835 1840
 Gly Leu Phe Ser Tyr Asp Gly Tyr Val Leu Asn Arg Ile Lys Asn Met
 1845 1850 1855
 Ile Thr Gln Asn Gln Ile Asn Asn Asp Ile Val Lys Val Ile Ser Asp
 1860 1865 1870
 Ile Glu Asn Phe Phe Lys Ile Cys Val Pro Phe Ser Lys Lys Glu Tyr

1875	1880	1885
Ala Leu Tyr Gly Val Thr Glu Thr Ala Leu Ser Ala Gly Met Asp Ala		
1890	1895	1900
Ile Glu Arg Trp Asn Lys Ala Val Glu Glu Glu Thr Asn Lys Ile Arg		
1905	1910	1915
Lys Glu Cys Arg Asp Leu Thr Asp Thr Gly Ser Val Tyr Asp Met Asn		1920
	1925	1930
Ile Ile Cys Pro Gly Asp Tyr Met Ser Ser Val Gly Glu Gly Gly Asn		1935
	1940	1945
Gly Gly Cys Gly Gly Gly Ser Ser Ser Ser Gly His Leu Leu Ser Asn		1950
	1955	1960
Asn Asn Asn Glu Ala Asn Gln Thr Asn Glu Ile Ser Glu Asp Gln Leu		1965
	1970	1975
Lys His Glu Gly Ser Asp Cys Ser Phe Trp Phe Asn Phe Tyr Lys Lys		1980
1985	1990	1995
Val Val Asn Ser Ser Glu Lys Lys Gln Gly Lys Gly Ser Val Leu Ala		2000
	2005	2010
Asn Thr Gly His Glu Gly Arg Ile Val Gly Arg Pro Leu Arg Thr Phe		2015
	2020	2025
Ile Gln Tyr Lys Gly Lys Gly Phe Ala Glu Thr Lys Val Leu Thr Arg		2030
	2035	2040
Tyr Phe Ser Asn His Asp Ser Tyr Trp Ser Gln Val Met Pro Ile Cys		2045
	2050	2055
Tyr Ile Lys Asn Met Ala Leu Gly Asp Glu Asp Lys Ser Lys Lys Lys		2060
2065	2070	2075
Phe Gly Lys Arg Pro Trp Lys Asn Phe Asn Asn Asn Ser Asn Ser Ser		2080
	2085	2090
Ser Asn Ser Ser Val Lys Tyr Val Ser Ile Gln Asp Leu Glu Lys Lys		2095
	2100	2105
Asp Ser Leu Lys Asn Val Pro Met Gly Tyr Asp Glu Asp Leu Leu Ser		2110
	2115	2120
Leu Tyr Asp Asp Ser Leu Thr Ser Thr Glu Lys Leu Glu Asn Ile		2125
	2130	2135
Lys Ile Val Asn Asp Ser Lys Asp Ala Tyr Val Ile Leu Gly Ser Ser		2140
2145	2150	2155
Asn Gln Ser Ser Phe Asp Gln Thr Phe Ser Gln Gln Tyr Phe Thr His		2160
	2165	2170
Gln Lys Ile Ser Asn Ile Asn Thr Tyr Lys Ser Leu Gly Lys Met Trp		2175
	2180	2185
Asn Cys Asn Asn Gly Met Ser Pro Lys Asn Gln Ile Val Leu Leu Lys		2190
	2195	2200
Lys Leu Leu Phe Lys Asn Leu Asn Ile Leu Trp Ile Lys Leu Tyr Glu		2205
	2210	2215
Arg His Val Leu Cys Asn Trp Gly Cys Ile His Pro Asn Ser Ser Lys		2220
2225	2230	2235
Asn Ser His Phe Glu Met Thr Lys Asn Asn Ala Pro Cys Gly Val Thr		2240
	2245	2250
Asp Ser Asn Pro Pro Leu Ser Val Tyr His Ser Gly Phe Leu Ser Val		2255
	2260	2265
Glu Asp Tyr Gly Gln Leu Leu Lys Asp Thr Phe Pro Leu Met Asn Leu		2270
	2275	2280
His Arg Thr Phe Ser Ala Lys Ser Lys Asp Asn Asn Ser Ser Asp Pro		2285
	2290	2295
Ser Pro Glu Lys Ile Ser Ala Ala Ser Leu Ala Lys Ala Val Tyr Ala		2300
2305	2310	2315
Arg Glu Val Leu Ser Ser Cys Leu Asp Pro Glu Gly Asn Phe Cys Thr		2320
	2325	2330
Ser Trp Ile Thr Asn Ser Cys Ser Val Leu Phe Thr Pro Gly Thr Asn		2335
	2340	2345
Ile Arg Arg Gly Gly Asp Phe Phe Asn Lys Ser Cys Tyr Arg Gln Gln		2350
	2355	2360
		2365

Asp Asn Asp Tyr Cys Phe Ile Gly Lys Glu Glu Thr Lys Lys Cys Pro
 2370 2375 2380
 Asn Phe Val Ser Ser Glu Ile Glu Ile Val Ser Ile Leu Lys Thr Ala
 2385 2390 2395 2400
 Val Phe Leu Ser Thr Asn Ser Asp Gly His Lys Arg Val Leu Arg Val
 2405 2410 2415
 Ile Asn Tyr Asn Lys Asp His Ser Gly Ala Gly Ile Asp Thr Gly Cys
 2420 2425 2430
 Ala Asp Asp Glu Asp Asp Asp Asp Asp Gln Gly Gly Thr Asp Lys Thr
 2435 2440 2445
 Cys Leu Leu Gln Glu Asp Ser Met Asp Ala Lys Arg Met Leu Ile Ser
 2450 2455 2460
 Met Arg Ser Val Ile Asn Gly Lys Ser Leu Asp Glu Ser Ser Leu Ala
 2465 2470 2475 2480
 Ile Lys Lys Asp Asn Phe Asn Phe Leu Ala Gly Thr Asp Lys Gly Phe
 2485 2490 2495
 Tyr Leu Asp Asn Ser Phe Phe Asn Ser Pro Val Gln Gly Lys Phe Val
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 Ala Pro Arg Gly Thr Lys Ile Phe Lys Lys Cys Cys Asp Phe Leu Leu
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 Ser Met Phe Asp Asn Glu Ser Glu Gln Gly Glu Leu Phe His Asp Arg
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 Tyr Cys Pro Asp Phe Leu Ser Asp Tyr Asn Lys Gln Asn Ile Phe Ser
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 Lys Asn Met Leu Lys Arg Ala Lys Asn Ile Arg Leu Cys Ile Thr Asn
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 Gly Asn Ala Arg Thr Phe Ile Ser Asn Gly Thr Ala Ile Pro Phe Arg
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 Leu Ala Glu Asn Thr Ala Cys Ile Ser Val Asp Asn Asn Arg Tyr Phe
 2675 2680 2685
 Leu Ile Asp Gly Thr Tyr Leu Leu Gly Gly Arg Leu Glu Gly Ile Asn
 2690 2695 2700
 Leu Val Thr Asp Met Tyr Thr Arg Cys Lys Leu Lys Ala Glu Lys His
 2705 2710 2715 2720
 Val Ile Leu Asn Ser Leu Phe Ser Thr Glu Phe Ile Ser Ala Ala Ser
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 Ser Met Glu Gly Thr Thr Met Gly Arg Gly Leu Cys Leu Ile Glu His
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 Val Ser Tyr Met Lys Asn Thr Asp Ser Val Ser Asn Met Asn Lys Asn
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 Phe Trp Ser Met Ala Glu Asp Gln Glu Glu Thr Asp Glu Asn Glu Asp
 2770 2775 2780
 Asp Asp Asp Glu Asn Glu Glu Asp Glu Asp Glu Asn Glu Glu Asn Thr
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 Glu Asn Thr Ser Val Val Lys Tyr Glu Pro Val Ser Lys Thr Ala Phe
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 Ser Ser Ser Leu Lys Pro Pro Ser Ile Phe Ile Ala Asp Glu Asp Tyr
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 Glu Thr Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser

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Ser Lys His Ser Ser Ser Ser Ser Ser Ser Asn Lys Lys Arg Lys Gln				
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Lys Asp Asp Val Asn Ser Thr Thr Thr Ala Leu His Ala Leu Arg Lys				2880
	2885		2890	2895
Cys Tyr Ile Ser Cys Val Asp Gln Lys Thr Gly Met Pro Arg Met Asp				
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Val Val Tyr Leu Leu Arg Gly Leu Met Asn Phe Gly Gly Met Cys Thr				
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Ala Ile Ala Ser Gly Asp Gly Glu Lys Ala His His Met Val Gln Thr				
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Leu Cys Ser Val Asn Ile Ala Thr Lys Thr Ala Val Val Phe Val Gly				
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Thr Lys Gly Asn Asn Leu Lys Thr Thr Leu Val Asp Leu Cys Lys Arg				2960
	2965		2970	2975
Thr Trp Phe Glu Arg Phe Thr Asn Ile Asn Val Thr Ala Leu Asn Asn				
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Ala Gly Asp Ser Ser Ser Ser Thr Gln Ala Asn Leu Ala Ser Phe Ala				
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Gly Lys Lys Gly Ile Val Ile Ile Asp Glu Val Gly His Gln Gly Ser				
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Phe Gly Ser Lys Lys Ser Ser Ser Glu Asp Asp Lys Asp Glu Ser Ala				
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Ser Arg Ser Gly Asn Val Asp Phe Gly Gly Ser Gly Gly Glu Met Asn				
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Ser Val Asp Ile Asn Glu Ala Arg Asn Ala Tyr Gly Asp Gly Gly Asn				
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Ser Lys Ile Val Phe Ser Asn Ile Asn Arg Leu Met Thr Glu Ser Lys				
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Leu Lys Val Cys Asp Gln Glu Tyr Asp Phe Ile Ser Glu Leu Lys His				
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Glu Lys Asn Arg Lys Asn Ala Cys Asn Asp Thr Lys Lys Arg Lys Arg				
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Gly Gly Glu Ile Glu Asp Glu Gly Val Glu Cys Glu Glu Ile Glu Arg				
	3125		3130	3135
Asn Asp Gly Lys Asn Asp Glu Asn Gly Val Arg Ile Lys Asp Pro Ile				
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Asn Ile Ser Phe Phe Ala Arg Lys Ala His Trp Trp Asn Cys Ser Ser				
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Gly Val Val Ser Thr Thr Phe Lys Glu Lys Asn Ile Val Tyr Asn Met				
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Leu His Arg Gly Ala Met Pro Phe Ser Ile Lys Asp Cys Thr Asp Ser				
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Pro Trp Leu Asn Glu Thr Asp Ala Val Tyr Arg His Cys Lys Lys Pro				
	3205		3210	3215
Ile Glu Tyr Glu Gly Lys Phe Ser Lys Ser Glu Val Lys Thr Ala Leu				
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Lys Cys Ile Leu Gly Lys Phe Gly Ser Lys Ile Cys Asp Asn Glu Ser				
	3235		3240	3245
Phe Glu Ser Ile Ile Asp Glu Asn Cys Gln Val Asn Asn Leu His Ser				
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Trp Asn Asp Cys Lys Glu Asp Ile Asp Glu Trp Asn Glu Lys Phe Met				
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Ser Lys Asn Lys Lys Asn Lys Gln Asn Met Lys Ile Glu Asp Lys Val				
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Asp Ala Ile Met Asn Ile Ile Gln Lys Asn Asn Gly Leu Leu Lys Trp				
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Ala Thr Glu Arg Phe Ser Glu Met Ile Thr Ser Ser Leu Ser Ala Gln				
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 Ala Ile Pro Gln Lys Asn Asp Val Ser Ser Ser Ile Thr Lys His Met
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 Pro Ala Asn Tyr Glu Ser Met Cys Asn Lys Leu Pro Ser Pro Leu Gln
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 Gly Arg Asp Phe Asn Ile Lys Met His Ser Pro Ala Thr Lys Asn Arg
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 Val Arg Asp Leu Met Tyr Ser Cys His His Leu His Met Leu Phe Glu
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 Thr Leu Lys Ser Asp Lys Thr Gly Val Asp Tyr Val Ala Val Met Leu
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 Ala Cys Met Val Tyr Gln Leu Met Val Ser Asn Leu Lys Tyr Pro Val
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 Phe Leu Ser Ser Ser Ser His Lys Arg Ala Asn Thr Glu Asp Ile Ala
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 Asp Glu Asn Gln Val Ser Ser Leu Ser Val Pro Met Phe Leu Ala Met
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 Val Val Asn Lys Pro Leu His Ala Leu Arg His Ser Thr Asn Leu Ala
 4100 4105 4110
 Leu Pro Asn Ala Ser Gln Lys Ser Asp His Ser Asp Ile Val Lys Tyr
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 Ser Cys Ser Arg Glu Thr Phe Asn Ser Val Lys Ala Ile Gln Tyr Phe
 50 55 60
 Asn Lys Thr Ser Arg Asn Asn Thr Ala His His Phe Lys Met Pro Ala
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<210> 171

<211> 1227

<212> PRT

<213> SHRIMP

<400> 171

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Gly Trp Thr Lys Lys Ala Ala Ala Asp Thr Asp Thr Pro Thr Ala
35     40     45
Lys Pro Thr Gly Leu Ser Ile Ser Leu Met Asp Ile Ser Gly Ser Met
50     55     60
Gly Ser Val Lys Ser Ala Val Ala Asp Ser Cys Ser Gly Ile Met Ala
65     70     75     80
Thr Leu Asn Val Ile Ala Pro Gly Ile Gln Asn Ala Ile Val Tyr Tyr
85     90     95
Asn Asp Phe Asp Lys His Ser Ile Glu Ser Gly Pro Val Val Arg Ala
100    105    110
Pro Asp Cys Ser Glu Trp Glu Gly Gly Asp Phe Val Lys His Met Arg
115    120    125
Lys Thr Glu Val Cys Gly Gly Gly Gly Gly Ser Glu Ala Leu His
130    135    140
Ser Ser Leu Met Tyr Val Phe Asn Asn Met Ile Pro Ala Phe Lys Lys
145    150    155    160
Met His Gly Ile Thr Arg Asp Glu Lys Phe Pro Ile Leu Ile Phe Val
165    170    175
Phe Thr Asp Glu Asp Val Arg Ile Ala Asn Ser Asp Thr Gly Lys Leu
180    185    190
Cys Ala Asn Ser Tyr Asp Ser Glu Thr Ala Pro Glu Glu Glu Phe Ile
195    200    205
Met Lys Thr Trp Gly Gln Lys Pro Leu Thr Ile Leu Asp Met Arg Lys
210    215    220
Ala Leu Val Glu Asn Asp Cys Trp Leu Arg Ile Leu Asn Phe Ser Arg
225    230    235    240

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Cys	Ser	Gly	Ser	Asn	Gln	Ser	Glu	Leu	Cys	Gln	Glu	Asp	Val	Ile	Asn
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Phe	Ser	Gly	Tyr	Asp	Asn	Asn	Arg	Trp	Gln	Leu	Phe	Glu	Ser	Phe	Asp
			260					265					270		
Arg	Arg	Ser	Cys	Asn	Val	Arg	Lys	Asn	Ile	Ala	Thr	Phe	Ile	Met	Arg
		275					280					285			
Gln	Ser	Ile	Ser	Leu	Phe	Lys	Asn	Leu	Asn	Asp	Gln	Phe	Ser	Ala	Phe
	290					295					300				
Pro	Ile	Leu	Arg	Glu	Ile	Asn	Gln	Glu	Glu	Leu	Asn	Val	Phe	Ile	Glu
305					310					315					320
Ser	Glu	Gly	Arg	Ser	Glu	Pro	Ala	Gly	Phe	Glu	Lys	Tyr	Gly	Asp	Ala
				325					330					335	
Gln	Arg	Glu	Ser	Phe	Lys	Ser	Arg	Val	Leu	Asn	Met	Ala	Pro	Leu	Asp
			340					345					350		
Phe	Gly	Arg	Val	Val	Gln	Gly	Gly	Gly	Arg	Tyr	Asn	Asn	His	Lys	Arg
		355				360						365			
Ser	Val	Phe	Leu	Asn	Cys	Ala	Tyr	Asp	Ser	Ala	Phe	Cys	Cys	Ser	Lys
	370					375					380				
Gln	Thr	Phe	Asn	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Ser	Ser	Ser
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Gly	Gly	Gly	Gly	Ile	Ser	Lys	Leu	Ala	Val	Val	Thr	Gln	Arg	Ala	Gln
				405					410					415	
Ser	Ile	Thr	Gly	Gly	Gly	Asn	Ala	Ala	Ser	Thr	Leu	Ala	Leu	His	Met
			420					425					430		
Asn	Ala	Cys	Phe	Gln	Ser	Leu	Asp	Asp	Phe	Gly	Ile	Asp	His	Thr	Asn
		435					440					445			
Leu	Cys	Asp	Cys	Lys	Gly	Cys	Thr	Lys	Leu	Met	Ala	Ser	Val	Glu	Ala
	450					455					460				
Thr	Ser	Asp	Gln	Gly	Arg	Lys	Thr	Lys	Leu	Ser	Arg	Lys	Tyr	Ala	Arg
465					470					475					480
Val	His	Trp	Ala	Lys	Met	Phe	Ala	Glu	Lys	Leu	Phe	Lys	Met	Met	Ile
				485					490					495	
Lys	Glu	Gln	Ser	Met	Met	Tyr	Ala	Cys	Ser	Ala	Val	Pro	Asp	Glu	Ile
			500					505					510		
Gly	Ala	Ile	Tyr	Ala	Phe	Val	Thr	Gly	Asn	Asn	Ala	Gly	Val	Cys	Ser
		515					520					525			
Arg	Val	Ser	Thr	Ile	Leu	Ser	Asp	Leu	Gly	Thr	Glu	Cys	Gly	Asn	Lys
	530					535					540				
Ala	Glu	Tyr	Ala	Phe	Leu	Lys	Glu	Gly	Lys	His	Met	Lys	Ser	Ala	Ser
545					550					555					560
Tyr	Asp	Ala	Leu	Gln	Val	Ile	Asn	Asn	Thr	Asp	Leu	Thr	Pro	Glu	Gln
				565					570					575	
Ser	Ser	Met	Phe	Met	Trp	Phe	Tyr	Val	Pro	Asn	Asp	Ala	Leu	Glu	Glu
			580					585					590		
Ala	Gly	Lys	Ile	Phe	His	Gln	Ser	Phe	Ser	Phe	Ser	Asn	Ser	Tyr	Thr
		595					600					605			
Gly	Gly	Gly	Leu	Leu	Ser	Leu	Asp	Glu	Tyr	Lys	Arg	Phe	Glu	Phe	Gly
	610					615					620				
Gln	Cys	Phe	Asp	Phe	Ile	Lys	Lys	Leu	Val	Ser	Cys	Leu	Lys	Ile	Thr
625					630					635					640
Arg	Asn	Val	Glu	Asp	Val	Leu	Leu	Glu	Thr	Ser	Lys	Thr	Ser	Asn	Arg
				645					650					655	
Tyr	Phe	Ala	Ile	Pro	Val	Phe	Cys	Gly	Ser	Asp	Asp	Gln	Lys	Glu	Val
			660					665					670		
Leu	Arg	Glu	Glu	Leu	Ala	Ser	Asp	Leu	Phe	Gly	Gly	Arg	Glu	Asp	Val
		675					680					685			
Ala	Glu	Met	Met	Phe	Ile	Asp	Leu	Glu	Thr	Val	Ile	Gln	Lys	Leu	Gly
	690					695					700				
Thr	Leu	Tyr	Asp	Val	Arg	Leu	Ser	Leu	Pro	Glu	Gly	Gly	Tyr	Ala	Ala
705					710					715					720
Ile	Lys	Ser	Val	Cys	Ala	Ala	Ala	Ser	Trp	Ala	Ala	Ser	Cys	Glu	Val

Pro	Ser	Asn	Thr	Ser	Asn	Met	Ile	Leu	Ser	Ile	Ala	Lys	Met	Ala	Phe	
			740					745					750			
Thr	Lys	Tyr	Tyr	Gln	Glu	Gln	Asn	Ser	Ser	Ser	Glu	Thr	Asp	Leu	Asp	
		755					760					765				
Ile	Ile	Leu	Pro	Ser	Ile	Gly	Thr	Ala	Asp	Gly	Glu	Ile	Glu	Asn	Asn	
	770					775					780					
Leu	Ser	Gly	Val	Val	Phe	Leu	Arg	Cys	Leu	Ile	Thr	Trp	Ala	Asn	Lys	
785					790					795					800	
Ile	Gly	Val	Asp	Lys	Asn	Phe	Thr	Asn	Lys	Leu	Glu	His	Phe	Leu	Ala	
				805					810					815		
Leu	Arg	Ile	Leu	Thr	Lys	Ala	Gly	Asp	Ser	Lys	Ile	Gly	Glu	Lys	Tyr	
			820					825					830			
Glu	Thr	Phe	Pro	Val	Arg	Arg	Leu	Asp	Leu	Ser	Glu	Lys	Asp	Leu	Lys	
		835					840					845				
Tyr	Ile	Cys	Lys	Arg	Cys	Gly	Val	Lys	Ser	Leu	Lys	Met	Glu	Tyr	Asp	
	850					855					860					
Asn	Asp	Glu	Lys	Leu	Cys	Leu	Arg	Cys	Lys	Gly	Asn	Tyr	Arg	Met	Gly	
865					870					875					880	
Lys	Pro	Met	Val	Tyr	His	Trp	Asp	Asn	Lys	Leu	Thr	Arg	Asp	Pro	Arg	
			885					890						895		
Ala	Lys	Thr	Asp	Thr	Thr	Leu	Asn	Leu	Leu	Asn	Ala	Lys	Lys	Ile	Asp	
			900					905					910			
Asp	Lys	Val	Lys	Glu	Met	Ala	Ser	Asp	Ile	Ile	Gly	Ala	Leu	Asn	Leu	
		915					920					925				
Pro	Pro	Thr	Asp	Lys	Asp	Asn	Glu	Ile	Ala	Val	Ser	Ala	Ala	Ala	Lys	
	930					935				940						
Ala	Val	Gly	Ile	Leu	Tyr	Gly	Lys	Thr	Cys	Leu	Leu	Tyr	Lys	Leu	Leu	
945					950					955					960	
Asn	Glu	Gly	Asn	Ile	Asp	Ile	Pro	Val	Ala	Val	Cys	Val	Glu	Cys	Asp	
			965						970					975		
Cys	Cys	Lys	Ser	Lys	Tyr	Met	Met	Ser	Thr	Leu	Gly	Pro	Asp	Lys	Pro	
			980					985					990			
Gln	Asn	Arg	Lys	Cys	Pro	Trp	Cys	Arg	Tyr	Ala	Asn	Lys	Leu	Val	Ala	
		995					1000					1005				
Met	Gly	Arg	Gly	Gly	Lys	Lys	Leu	Leu	Met	Asp	Leu	Ile	Glu	Cys	Gly	
	1010					1015					1020					
Ala	Pro	Ser	Leu	Ala	Met	Val	Glu	Glu	Ala	Ile	Arg	Thr	Ser	Gly	Asp	
1025					1030					1035					1040	
Val	Met	Tyr	Glu	Glu	Leu	Gly	Glu	Gly	Glu	Glu	Phe	Tyr	Ile	Ile	Asp	
			1045						1050					1055		
Tyr	Phe	Leu	Lys	Leu	Lys	Asn	Thr	Ala	Ile	Ala	Glu	Gly	Asn	Lys	Leu	
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<210> 172
<211> 294
<212> DNA
<213> SHRIMP

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agagaagctg tcttttagacg gcttctagaa gaagaaagga aaaaacacga agacgaggtg 180
ggagatgtgg aagataaaaag acaagcagtg atagacaagg caaatacaat gattacaaca 240
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<210> 173
<211> 93
<212> PRT
<213> SHRIMP

<400> 173
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20 25 30
Gly Leu Ile Pro Ser Ile Arg Glu Ala Val Phe Arg Arg Leu Leu Glu
35 40 45
Glu Glu Arg Lys Lys His Glu Asp Glu Val Gly Asp Val Glu Asp Lys
50 55 60
Arg Gln Ala Val Ile Asp Lys Ala Asn Thr Met Ile Thr Thr Met Ala
65 70 75 80
Ala Glu Tyr Leu Glu Ser Val Asp Ile Glu Phe Gly Phe
85 90

<210> 174
<211> 1530
<212> DNA
<213> SHRIMP

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ttgcataaaa atactccaaa acatgaggtg gatgaaattg tgaataaaaat acgcctctca 180
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gatttgagga atatcaacaa tatagtgaag agagaagctt taccatga caagtctttc 360
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agttgtcatg accaatgctt agttgttcca gtgagtatgt tagggaagat tttttcaagt 660
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<210> 175

<211> 507

<212> PRT

<213> SHRIMP

<400> 175

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 20          25          30
Ala Glu Gly Val Tyr Ile Val Ser Leu His Lys Asn Thr Pro Lys His
 35          40          45
Glu Val Asp Glu Ile Val Asn Lys Ile Arg Leu Ser Ala Gly Asn Pro
 50          55          60
Cys Leu Glu Lys Thr Ser Leu Phe Leu Gln His His Ser Gln Met Arg
 65          70          75          80
Asn Phe Tyr Thr Arg Lys Gly Ala Glu Ser Glu Ser Asp Trp Leu Lys
 85          90          95
Arg Leu Pro Glu Asp Leu Arg Asn Ile Asn Asn Ile Val Lys Arg Glu
100          105          110
Ala Leu Pro His Asp Lys Ser Phe Thr Phe Ser Pro Leu Tyr Arg Ile
115          120          125
Leu Thr Asp Arg Leu Phe Asn Ala Ala Ile His Asn Cys Lys Tyr Ile
130          135          140
Ile Val Thr Ala Asp Leu Leu Met Gly Cys Gly Ile Thr Asn Asn Lys
145          150          155          160
Val Glu Lys Lys Leu Leu Ser Met Gly Ser Ile Leu Gly Gly Glu Ser
165          170          175
Met Val Pro Leu His Asp Ile Ala His Arg Leu Ser Tyr Lys Gly Leu
180          185          190
Arg Ile Glu Asn Pro Ile Val Gly Ser Cys His Asp Gln Cys Leu Val
195          200          205
Val Pro Val Ser Met Leu Gly Lys Ile Phe Ser Ser Asn Met Tyr Pro
210          215          220
Thr Phe Lys Asn Phe Asp Gln Cys Met Ala Leu Phe Leu Asn Ala Val
225          230          235          240
Val Thr His Ser Ala Glu Lys Met Asp Gly Lys His Glu Arg Asn Lys
245          250          255
Val Ile His Met Pro Asn Glu Val Tyr Leu Asp Ala Ala Arg Arg Lys
260          265          270
Tyr Leu Glu Glu Lys Leu Glu Glu Thr Asn Lys Leu Asp Ala Ile Asp
275          280          285
Glu Glu Ala Arg Glu Glu Tyr Gly Asn Glu Ile Gly Arg Ile Gly Asp
290          295          300
Lys Ser Thr Cys Leu Val Phe Ala Leu Ser Ala Arg Asp Phe Phe Leu
305          310          315          320
Thr Asn Arg Phe Asn Glu Asp Thr Pro Lys Gly Thr Glu Arg Gly Ile
325          330          335
Arg Phe Met Cys Ser Asn Tyr Cys Thr Met Arg Asp Glu Gly Gly Phe
340          345          350
Arg Pro Arg Leu Ile Met Ser Ala Tyr Gly Pro Thr Ser Tyr Pro Ile
355          360          365
Ile Phe Asn Thr Leu Tyr Asp Gln Phe Asn Val Gln Tyr Tyr Pro Cys

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WO 01/38351

PCT/US00/28888

265

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Val Ser Gly Val Val Leu Ser Phe Ile Gly Asp Asp Gln Leu Ala Pro
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Glu Pro Glu Ser Leu Val Asp Ile Val Val Arg Ser Ile Lys Asn Pro
      405              410              415
Ser Ile Arg Ile Phe Ser Gly Asp Gly Glu Thr Val Tyr Gln Asp Gly
      420              425              430
Arg Arg Val Asp Val Gly Gly Glu Gly Lys Asn Gln Lys Phe Asn Arg
      435              440              445
Glu Glu Arg Thr Ile Leu Asn Val Leu Arg Ile Ile Lys Ala Tyr Asn
      450              455              460
Glu Glu Arg Thr Lys Glu Asp Glu Asp Glu Glu Glu Glu Glu Glu
465              470              475              480
Glu Glu Glu Gln Gln Thr Ala Ala Thr Val Thr Val Glu Ser Asp Trp
      485              490              495
Asp Leu Ser Leu Glu Arg Gly Glu Asn Trp Val
      500              505

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<210> 176
 <211> 246
 <212> DNA
 <213> SHRIMP

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<400> 176
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aaaaactttt caaaaatttt ttcagctcac tccagtttag ggggtggacc gctgactagg 180
ccttatgtca agttcgaagg gtggaccgct gggtcgaccc aacgtcagat tacagagagg 240
agctag                                     246

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<210> 177
 <211> 77
 <212> PRT
 <213> SHRIMP

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<400> 177
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Asn Thr Ala Asp Pro Gly Gly Leu Ser Tyr Pro Phe Asn Pro Leu Phe
      20          25          30
Thr Leu His Leu His Leu Lys Asn Phe Ser Lys Ile Phe Ser Ala His
      35          40          45
Ser Ser Leu Gly Gly Gly Pro Leu Trp Tyr Val Lys Phe Glu Gly Trp
      50          55          60
Thr Ala Gly Ser Thr Gln Arg Gln Ile Thr Glu Arg Ser
65          70          75

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<210> 178
 <211> 738
 <212> DNA
 <213> SHRIMP

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<400> 178
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gaatcagtag aaacacacccc gccgagtaag ctccccagag tcgatgaaga tgaagtctat 180
attgatgaaa atgttgatgg tgatgtgcag atcctcgcct catcaatcga agtcgccaga 240
atggagagag aaagacttgc cgaagccatg gtccgagaca taaaaatcga ggaagaaaaa 300
gccgcaacgg aagcgaggaa agaaatagcc tctcgccataa tttataaaga aatggtatat 360

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cttttgccctc aactggaaaa catgactaac cgcctccgtc cgagatcact tctcaggcac 420
aacgaaatga ccattacaga ccgcacgttc agtgatttgc agatattcaa caaagtcact 480
tttgaattcc ctatactgac tgatattgct ttccttgccc gtgaaaaatc acgtgtcgag 540
ggttcgagat tctacaacga tatgaagatt ggacctataa cagcctacaa attgaatttg 600
atgtgtaata aattcataga gtctgttggtg caaaagggtga aggcagaaat atccccattt 660
gttgaagtta gtgtatcaag tgaacttgaa gggtcacctt tttgggattt caagcaaaga 720
atagtaaaac acacctag                                     738

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<210> 179

<211> 245

<212> PRT

<213> SHRIMP

<400> 179

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Met Val Ser Thr Arg Ser Met Glu Ala Lys Ala Ala Ala Ala Lys
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Ala Lys Glu Val Ser Pro Thr Thr Ser Lys Arg Lys Ala Glu Asp Leu
20     25     30
Thr Glu Gly Thr Glu Glu Glu Glu Ser Val Glu Thr His Pro Pro
35     40     45
Ser Lys Leu Pro Arg Val Asp Glu Asp Glu Val Tyr Ile Asp Glu Asn
50     55     60
Val Asp Gly Asp Val Gln Ile Leu Ala Ser Ser Ile Glu Val Ala Arg
65     70     75     80
Met Glu Arg Glu Arg Leu Ala Glu Ala Met Val Arg Asp Ile Lys Ile
85     90     95
Glu Glu Glu Lys Ala Ala Thr Glu Ala Arg Lys Glu Ile Ala Ser Arg
100    105    110
Leu Ile Tyr Lys Glu Met Val Tyr Leu Leu Pro Gln Leu Glu Asn Met
115    120    125
Thr Asn Arg Leu Arg Pro Arg Ser Leu Leu Arg His Asn Glu Met Thr
130    135    140
Ile Thr Asp Arg Thr Phe Ser Asp Leu Gln Ile Phe Asn Lys Val Thr
145    150    155    160
Phe Glu Phe Pro Ile Leu Thr Asp Ile Ala Phe Leu Ala Arg Glu Lys
165    170    175
Ser Arg Val Glu Gly Ser Arg Phe Tyr Asn Asp Met Lys Ile Gly Pro
180    185    190
Ile Thr Ala Tyr Lys Leu Asn Leu Met Cys Asn Lys Phe Ile Glu Ser
195    200    205
Val Val Gln Lys Val Lys Ala Glu Ile Ser Pro Phe Val Glu Val Ser
210    215    220
Val Ser Ser Glu Leu Glu Gly Ser Pro Phe Trp Asp Phe Lys Gln Arg
225    230    235    240
Ile Val Lys His Thr
245

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<210> 180

<211> 1221

<212> DNA

<213> SHRIMP

<400> 180

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gcttctgctg ttacaagtat caactctaata tctacgtctt cttctgcaat gttccgagta 180
ccacaaggta tctctgttac ggccatgcct cccgtgccag cacttacatc tctgactgaa 240
tctactggaa cgaggatgtc ttctacaccc aatgtggatg ttatacctgt tcctggcccc 300
aagaacaagt ccaagtctaa gaagaaggat tcaaagagga agaagaacca gaatggcaac 360
cgtagcagtg acgaggacga accatctctt gttatcgacg acggttcttg aagacagtct 420

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aagaacaaga aatattcttg ggtcacatct cttgctacta ctacggctga aagaacaac 480
gacactctcg cccacactag gcccttcctt cccacacccg aagaaggaaa tatgtctgaa 540
attgacgcag ggctaagtaa tccagtcact cgccaaatca ccggagaagt ttatagcgct 600
gcactcactt ctggagttgg agataatgga ctatatcctt cccacttcac ggttgctgac 660
acttcttacg gagattgcga aacaccata cctggacctg cttttgtcct cgacgacggg 720
acagttagca gaggcacatc tcttctgcac agagaagagg cagaattctt gaatgatgga 780
agtaagggtga tccataaccgt taaaccaaga aacagcaagt actccaatat tcaacgtgcc 840
gctagctgta tggcctacgc tgtggacctt ctaaacaacc ataatatcac ctctgaccaa 900
tttgatttta tggctatgac tgcattgggca gcccgtaac gttgtggaga aatggccaag 960
ttttttgaga agcgcgataa ggacatcgga gaatatagga ataagggtggt ccaatacaac 1020
agaggcatct ttacacgcac cactgaaatg aataaacgcg caaagattat cctggaacaa 1080
caacaacgcc gtgaagctgc tgccgctgcc gctgccaccg gtgccaccgc ccctatccct 1140
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<210> 181
 <211> 402
 <212> PRT
 <213> SHRIMP

<400> 181

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			20					25					30		
Ala	Ala	Ile	Ala	Ser	Arg	Thr	Ser	Ala	Ser	Ala	Val	Thr	Ser	Ile	Asn
		35					40					45			
Ser	Asn	Ser	Thr	Ser	Ser	Ser	Ala	Met	Phe	Arg	Val	Pro	Gln	Gly	Ile
	50					55					60				
Ser	Val	Thr	Ala	Met	Pro	Pro	Val	Pro	Ala	Leu	Thr	Ser	Leu	Thr	Glu
65					70					75					80
Ser	Thr	Gly	Thr	Arg	Met	Ser	Ser	Thr	Pro	Asn	Val	Asp	Val	Ile	Pro
				85					90					95	
Val	Pro	Gly	Pro	Lys	Asn	Lys	Ser	Lys	Ser	Lys	Lys	Lys	Asp	Ser	Lys
			100					105					110		
Arg	Lys	Lys	Asn	Gln	Asn	Gly	Asn	Arg	Ser	Ser	Asp	Glu	Asp	Glu	Pro
		115					120					125			
Ser	Leu	Val	Ile	Asp	Asp	Gly	Ser	Gly	Arg	Gln	Ser	Lys	Asn	Lys	Lys
	130					135					140				
Tyr	Ser	Trp	Val	Thr	Ser	Leu	Ala	Thr	Thr	Thr	Ala	Glu	Arg	Asn	Asn
145					150					155					160
Asp	Thr	Leu	Ala	Pro	Pro	Arg	Pro	Phe	Leu	Pro	Thr	Pro	Glu	Glu	Gly
			165					170						175	
Asn	Met	Ser	Glu	Ile	Asp	Ala	Gly	Leu	Ser	Asn	Pro	Val	Thr	Arg	Gln
		180						185					190		
Ile	Thr	Gly	Glu	Val	Tyr	Ser	Ala	Ala	Leu	Thr	Ser	Gly	Val	Gly	Asp
	195						200					205			
Asn	Gly	Pro	Ser	His	Phe	Thr	Val	Ala	Asp	Thr	Ser	Tyr	Gly	Asp	Cys
	210					215					220				
Glu	Thr	Pro	Ile	Pro	Gly	Pro	Ala	Phe	Val	Leu	Asp	Asp	Gly	Thr	Val
225					230					235					240
Ser	Arg	Gly	Thr	Ser	Leu	Leu	His	Arg	Glu	Glu	Ala	Glu	Phe	Leu	Asn
			245						250					255	
Asp	Gly	Ser	Lys	Val	Ile	His	Thr	Val	Lys	Pro	Arg	Asn	Ser	Lys	Tyr
		260						265					270		
Ser	Asn	Ile	Gln	Arg	Ala	Ala	Ser	Cys	Met	Ala	Tyr	Ala	Val	Asp	Leu
		275					280					285			
Leu	Asn	Asn	His	Asn	Ile	Thr	Ser	Asp	Gln	Phe	Asp	Phe	Met	Ala	Met
	290					295					300				
Thr	Ala	Trp	Ala	Ala	Arg	Gln	Arg	Cys	Gly	Glu	Met	Ala	Lys	Phe	Phe
305					310					315					320

[illegible]

<210>	182
<211>	1617
<212>	DNA
<213>	SHRIMP

<400>	182						
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ctaaaggaag	gacattttat	agttcgtctt	agagacaagg	aagtactcca	catcaagaac	180	
ggtaacgaa	gattgagaca	attaacagga	gatctacgc	ttcagattgg	actaaaatac	240	
acatccagtc	tcccaaaaca	aggtagtttc	ttagaagatg	aagaccctta	ttatggaaaa	300	
aaatggaacg	aatcactacc	aagcccattc	caggaaatga	acaaaattgt	ggaagaaaag	360	
gctctagtta	atgacaagaa	ctttaaattt	tcacccttat	acagaatcat	acatgaacgt	420	
ctttcaaatg	cggccgtaa	gaaatgtgat	tatatgataa	tcacaacaga	cttcttagta	480	
gggtgtgggt	tttctcctag	aaattgtacc	cgtactctta	agaatatgga	acaagtgtta	540	
gtgcaacacg	gtggtacctc	ttctcgtgta	tcagtgtatg	atatctgtga	taggttaacg	600	
tacaatggct	taagtatcgc	aaaccccata	gttggcagtt	tttcaaatac	gtgcctaatt	660	
gtaccaatgg	ataaacttgg	attacttttc	tacaacagca	cacacccgct	agctaaaagc	720	
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aatcaaaaaat	tagataattt	cgaaaaggaa	atcagatttg	caaaaaatga	agtcaacctt	840	
ctagtttagcg	aaagaagtgt	tctggaagaa	aaacttaaag	aatccaaaaa	gctatatgct	900	
gcctcagaag	aacaaaaggat	ttctcttcga	gatgtgcata	aaaagtcctc	aattgcatca	960	
tccagatatg	acggcgggtgc	ctgtctggtc	tttgcccttt	ctgaccgaga	tttctccttg	1020	
ttgtgcagaa	ccaatgaaa	tggttccttt	tactctgcc	cagaagaagg	aatcagatac	1080	
tctctctcgg	agcactacag	aaagagggac	gtggatgaac	gtaggccag	attggtcatg	1140	
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aaccatttca	ttgcatccgg	aaagggtaat	gaaatatcat	tcatcgatcc	tccgaatgaa	1260	
aggttgttga	tggagatgg	cagagagggt	actggatcag	acatcaaaat	cttcatggat	1320	
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ggcaagggaca	taataaaaaa	ggaagaaaaca	ttaccagagg	aggaaaaggaa	gcgtctgcgc	1440	
cgagagcgct	gcatgatttt	caacacagtt	aaggcaattg	agacgtacaa	cgagggaacgt	1500	
ggggagaag	aagaagtgc	cacaagcagt	ggaggaaaca	agagaaaag	ggaggagaaa	1560	
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<210> 183
<211> 534
<212> PRT
<213> SHRIMP
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<400> 183

Met	Glu	Asp	Phe	Lys	Gln	Leu	Lys	Val	Lys	Asn	Gly	Ile	Cys	Leu	Ser
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Gly	Glu	Asn	Thr	Glu	Asn	Tyr	Glu	Arg	Val	Leu	Leu	Thr	Phe	Lys	Ser
			20					25					30		
Val	Lys	Ser	Val	Arg	Arg	Ser	Glu	Leu	Lys	Glu	Gly	His	Phe	Ile	Val
		35					40					45			
Arg	Leu	Arg	Asp	Lys	Glu	Val	Leu	His	Ile	Lys	Asn	Gly	Asn	Glu	Arg

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[illegible]

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<210> 184
 <211> 1386
 <212> DNA
 <213> SHRIMP

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 atggatatcg aacctatggg actggccaag atctctactg gatatggaat agacaagttt 180
 cccgacggct gttatggaca aattgtgtca cgttctggga tgacatggaa gaacaacact 240
 agtgtaccta ctggaacgat tgatgtggat tataggggag aattgaaagt gattctgctc 300
 aacctatagt cagaaaaaag tgtgccaatc agaaaaggaa ccagcattgc ccagttgatt 360
 ttcttaagat attgtgatgt cgaggaagaa cagattgtgt atattaatga aaccacggga 420
 gagagaacga ttattgactc tagttctaaa aaggacaaca aaaatcaagc aagaagcgtg 480
 cgtggaactg gtggatttgg atctacagat aaccctaaatt ttactgaaac caccgtctca 540
 agaaaccaac aagaagagaa caaaaaggaa gaattggaag aaggggagat cgtagaaatg 600
 gaaggtttta ttgacattcc ttttcttgaa ggttttcgaaa atatcctcgc agaacaaagc 660
 aacgaaactg gtgtgacata ccctaatacg aatcaagatg tggaagaaaa agatactaaa 720
 aatatagatg tcgtcagaga attggaagct gaatttagta gtggaattgg gagtggctcc 780
 atggactctt ctgactcatc cgattcttct tcttcttctc ctgactcatc cgattcgtct 840
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 ataagacgtc atcagtatca ccggcgccag ttgagttatt cggatgacgt caatggaggg 960
 ggaagaaatt ctgagaaaaat ggagatggac agagtaactc acataaaaaac tgaacacata 1020
 aaaagagagg acgaacccag atacgaagaa agagaaagat atattcatcc aagaagaatg 1080
 caagtgccca aggactatta ttgtgagcaa tacgaacact acgacgcccc tgctgctgct 1140
 caccaccacc gccaccacca acaccgccac caaccaccaga ggcactttaa ccaaccccg 1200
 tccaacaatt cttctgacgt tactgcttac gtcaatgaaa attccccac gaggccatgc 1260
 cgtgatcgca actctcgatt ctcagaaaga cccaacaatg gcggttataa ccggatcaac 1320
 tcaaggata caactttcga cccttataga tatggcgcaa gaagagggcg tggaggagta 1380
 tattag 1386

<210> 185
 <211> 457
 <212> PRT
 <213> SHRIMP

<400> 185
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 Glu Glu Thr Ala Leu Pro Pro Arg Arg Ala Thr Pro Gly Ser Val Ala
 20 25 30
 Tyr Asp Leu Phe Pro Ser Glu Glu Met Asp Ile Glu Pro Met Gly Leu
 35 40 45
 Ala Lys Ile Ser Thr Gly Tyr Gly Ile Asp Lys Phe Pro Asp Gly Cys
 50 55 60
 Tyr Gly Gln Ile Val Ser Arg Ser Gly Met Thr Trp Lys Asn Asn Thr
 65 70 75 80
 Ser Val Pro Thr Gly Thr Ile Asp Val Asp Tyr Arg Gly Glu Leu Lys
 85 90 95
 Val Ile Leu Arg Asn His Ser Ala Glu Lys Ser Val Pro Ile Arg Lys
 100 105 110
 Gly Thr Ser Ile Ala Gln Leu Ile Phe Leu Arg Tyr Cys Asp Val Glu
 115 120 125
 Glu Glu Gln Ile Val Tyr Ile Asn Glu Thr Thr Gly Glu Arg Thr Ile
 130 135 140
 Ile Asp Ser Ser Ser Lys Lys Asp Asn Lys Asn Gln Ala Arg Ser Val
 145 150 155 160
 Arg Gly Thr Gly Gly Phe Gly Ser Thr Asp Asn Pro Asn Phe Thr Glu
 165 170 175

Thr Thr Val Ser Arg Asn Gln Gln Glu Glu Asn Lys Lys Glu Glu Leu
 180 185 190
 Glu Glu Gly Glu Ile Val Glu Met Glu Gly Phe Ile Asp Ile Pro Phe
 195 200 205
 Leu Glu Gly Phe Glu Asn Ile Leu Ala Glu Gln Ser Asn Glu Thr Gly
 210 215 220
 Val Thr Tyr Pro Asn Thr Asn Gln Asp Val Glu Lys Asp Thr Lys
 225 230 235 240
 Asn Ile Asp Val Val Arg Glu Leu Glu Ala Glu Phe Ser Ser Gly Ile
 245 250 255
 Gly Ser Gly Ser Met Asp Ser Ser Asp Ser Ser Asp Ser Ser Ser Ser
 260 265 270
 Ser Ser Asp Ser Ser Asp Ser Ser Asp Ser Ser Asp Ser Glu Ser Ser
 275 280 285
 Asp Asp Ser Glu Gly Gly Asp Asn Lys Val Arg Arg Ile Arg Arg His
 290 295 300
 Gln Tyr His Arg Arg Gln Leu Ser Tyr Ser Asp Asp Val Asn Gly Gly
 305 310 315 320
 Gly Arg Asn Ser Glu Lys Met Glu Met Asp Arg Val Thr His Ile Lys
 325 330 335
 Thr Glu His Ile Lys Arg Glu Asp Glu Pro Arg Tyr Glu Glu Arg Glu
 340 345 350
 Arg Tyr Ile His Pro Arg Arg Met Gln Val Pro Lys Asp Tyr Tyr Cys
 355 360 365
 Glu Gln Tyr Glu His Tyr Asp Ala Pro Ala Ala His His His Arg
 370 375 380
 His His Gln His Arg His Gln His Gln Arg His Phe Asn Gln Pro Arg
 385 390 395 400
 Ser Asn Asn Ser Ser Asp Val Thr Ala Tyr Val Asn Glu Asn Ser Pro
 405 410 415
 Trp Cys Arg Asp Arg Asn Ser Arg Phe Ser Pro Asn Asn Gly Gly Tyr
 420 425 430
 Asn Arg Ile Asn Ser Arg Tyr Thr Thr Phe Asp Pro Tyr Arg Tyr Gly
 435 440 445
 Ala Arg Arg Gly Arg Gly Gly Val Tyr
 450 455

<210> 186

<211> 1014

<212> DNA

<213> SHRIMP

<400> 186

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 gaacttgga tacctcttgt tgaaggaaag gaagtactac tggaatttgc ctacaaaata 180
 ttaacaaaaa gggacacaa acgtgtaatt ggtgacgagc aaggagacgt atgtagcgct 240
 ttctttcttc gttttggaaa gaagaagact tttaatccac aaacaaaaat gtggctagt 300
 aaactggcca atgctatcgc cctatccatg ggtgtgtgcc cagaacctgc ctgcacgtgt 360
 tccagaatga tgacgactgc aaagaagatc cctgttccag aatcatacaa aaatgttaat 420
 cgcaatatcc aaaaatttga agatgtacat tatatagata tcaattttca gtcctttgta 480
 agagaacaga taggtttaag tgtattaggt aaaaatgatg tccaaaagaa gaagaaggaa 540
 gaaacccctt tctttgcacc cttaataaaa tctaaaatag gaggtgaatg catagaagat 600
 ttaaagtatg attctgagtc tgtttctatt ataagagatg tgtttaattt attgggtgaa 660
 atgcctactg aggatgtaaa gacatcaaga agttgtataa acccttccca caatgatacg 720
 aatcctagta tgaggttagt gtttcgtccc atgtactgga gaaattctaa gctggctatg 780
 gataaattat ccaaggaaca agactcggct ttgattgaaa agtatatggg aggagaacat 840
 caacattgta tcattggagg gagaaatgta ttattgtatt gtataactgc actatgtttt 900
 agctctgatt gtggatttaa aaagatgtta actaatgatg aaataaaaca attgatatgg 960
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<210> 187
 <211> 335
 <212> PRT
 <213> SHRIMP

<400> 187
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 Pro Lys Cys Thr Ser Ser Ser Leu Ser Leu Glu Glu Ser Val Asp Tyr
 20 25 30
 Leu Glu Lys Asp Phe Glu Glu Leu Gly Ile Pro Leu Val Glu Gly Lys
 35 40 45
 Glu Val Leu Leu Glu Phe Ala Tyr Lys Ile Leu Asn Lys Arg Asp Thr
 50 55 60
 Ile Arg Val Ile Gly Asp Glu Gln Gly Asp Val Cys Ser Val Phe Phe
 65 70 75 80
 Leu Arg Phe Gly Lys Lys Lys Thr Phe Asn Pro Gln Thr Lys Met Trp
 85 90 95
 Leu Val Lys Leu Ala Asn Ala Ile Ala Leu Ser Met Gly Val Val Pro
 100 105 110
 Glu Pro Ala Cys Thr Cys Ser Arg Met Met Thr Thr Ala Lys Lys Ile
 115 120 125
 Pro Val Pro Glu Ser Tyr Lys Asn Val Asn Arg Asn Ile Gln Lys Phe
 130 135 140
 Glu Asp Val His Tyr Ile Asp Ile Asn Phe Gln Ser Phe Val Arg Glu
 145 150 155 160
 Gln Ile Gly Leu Ser Val Leu Gly Lys Asn Asp Val Gln Lys Lys Lys
 165 170 175
 Lys Glu Glu Thr Pro Phe Phe Ala Pro Phe Asn Lys Ser Lys Ile Gly
 180 185 190
 Gly Glu Cys Ile Glu Asp Leu Lys Tyr Asp Ser Glu Ser Val Ser Ile
 195 200 205
 Ile Arg Asp Val Phe Asn Leu Leu Gly Glu Met Pro Thr Glu Asp Val
 210 215 220
 Lys Thr Ser Arg Ser Cys Ile Asn Pro Ser His Asn Asp Thr Asn Pro
 225 230 235 240
 Ser Met Arg Leu Val Phe Arg Pro Met Tyr Trp Arg Asn Ser Lys Leu
 245 250 255
 Val Met Asp Lys Leu Ser Lys Glu Gln Asp Ser Ala Leu Ile Glu Lys
 260 265 270
 Tyr Met Gly Gly Glu His Gln His Cys Ile Ile Gly Gly Arg Asn Val
 275 280 285
 Leu Leu Tyr Cys Ile Thr Ala Leu Cys Phe Ser Ser Asp Cys Gly Phe
 290 295 300
 Lys Lys Met Leu Thr Asn Asp Glu Ile Lys Gln Leu Ile Trp Tyr Leu
 305 310 315 320
 Val Leu Leu Phe Phe His Ile Ile Cys Pro Ile Ile Gln Ser Lys
 325 330 335

<210> 188
 <211> 3627
 <212> DNA
 <213> SHRIMP

<400> 188
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 tgttcaggag aagaagattg cacaactagc tcacttctca aagccacttc tcttgccaac 180
 atcaactcca agaacttcct ggatttttga agaggcaaga aatcttcctc ttcttcacct 240

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acctgtgact acacactcga catggttgat ttgccactt ataatgtatc agatctggtc 300
atgttgggca ggcaattgac aaccaccatg ttgaaggagc agaaaaatat gggtcagatg 360
atcctgttta tcaatactac aaatcaacag ataatagacg ttttacatga cggttttaat 420
gttatcaggg aagaagatac tatgcattca cggatgcaga acaagaaaca tatttatgaa 480
aatttttact gcagggatga aaagaagggtt atttctgaat tcttttctag aaaatataaa 540
cacgagaaaa ttaaggctag aattgaaaga gtgcctatta taatcccttc atcccaagag 600
gaagtgtatt ggctaactga acctccaatc gaagacatga tgatggctcc tccagtttct 660
aatcacaaaa tggacgacta tgaggggtctc gattactgga tcaacaaaca cacagatgtt 720
atgaagaaga ggaagttttt gactaacagt ttcttgttca ggaacgtgcc tactacttca 780
ttcaattctt ccccgacagc agttttgaaa tccagattca aagatgcatt ttttgctagc 840
cagatggagg gggtcactct gtactacgct tttaggatga tccgagtgat gaaaaatctc 900
ctcaagtcta aaaaccttaa agggaggtat actgtactct ttacggatgg aaaggctcca 960
gccatcaaga tgatgacgag agccaaacga cagatcagac aagaaagaag taaggaaaaag 1020
gcaaaatcaa ggaatgaaaa ttgcctcaat aggaagacca acgatctact attctactcg 1080
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ttcaccgaag cagaggatga tatcgtagct ttaacatcat gccttttgaa tctggagact 1260
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atgtctggta acagaaaaga atccaagagg tgggaagatt tattgaatgt tttgaagcaa 1380
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ctggtgaaat ggaacctgat ggttgagcat cataaaaaacg tgtgtcgtct tactgtgaca 1500
caatttaagg actctgaaac gttcttaaaag attggccatg tcaagttctt taggtgcatg 1560
aacagtaatt cttcgggtga aaatcaagca aacgagttgg gtggttttgc agctaaaaaga 1620
agaacaaagc caaatacgat atataatttg gcagaatcgc cgctcatgct ttcacctgaa 1680
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<211> 1204

<212> PRT

<213> SHRIMP

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Asp	Asp	Glu	Asp	Asp	Glu	Asp	Tyr	Cys	Ser	Gly	Glu	Glu	Asp	Cys	Thr
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Thr	Ser	Ser	Leu	Leu	Lys	Ala	Thr	Ser	Leu	Ala	Asn	Ile	Asn	Ser	Lys
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Asn	Phe	Leu	Asp	Phe	Gly	Arg	Gly	Lys	Lys	Ser	Ser	Ser	Ser	Ser	Pro
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Thr	Cys	Asp	Tyr	Thr	Leu	Asp	Met	Val	Asp	Leu	Pro	Thr	Tyr	Asn	Val
				85					90					95	
Ser	Asp	Leu	Val	Met	Leu	Gly	Arg	Gln	Ile	Ala	Thr	Thr	Met	Leu	Lys
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Gly	Gln	Lys	Asn	Met	Gly	Gln	Met	Ile	Leu	Phe	Ile	Asn	Thr	Thr	Asn
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Gln	Gln	Ile	Ile	Asp	Val	Leu	His	Asp	Gly	Phe	Asn	Val	Ile	Arg	Glu
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Glu	Asp	Thr	Met	His	Ser	Arg	Met	Gln	Asn	Lys	Lys	His	Ile	Tyr	Glu
145					150					155					160
Asn	Phe	Tyr	Cys	Arg	Asp	Glu	Lys	Lys	Val	Ile	Ser	Glu	Phe	Phe	Ser
				165					170					175	
Arg	Lys	Tyr	Lys	His	Glu	Lys	Ile	Lys	Ala	Arg	Ile	Glu	Arg	Val	Pro
			180					185					190		
Ile	Ile	Ile	Pro	Ser	Ser	Gln	Glu	Glu	Val	Asp	Trp	Leu	Thr	Glu	Pro
		195					200					205			
Pro	Ile	Glu	Asp	Met	Met	Met	Ala	Pro	Pro	Val	Ser	Asn	His	Lys	Met
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Met	Lys	Lys	Arg	Lys	Phe	Leu	Thr	Asn	Ser	Phe	Leu	Phe	Arg	Asn	Val
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Pro	Thr	Thr	Ser	Phe	Asn	Ser	Ser	Pro	Thr	Ala	Val	Leu	Lys	Ser	Arg
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Phe	Lys	Asp	Ala	Phe	Phe	Ala	Ser	Gln	Met	Glu	Gly	Val	Ile	Leu	Tyr
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Ala	Ile	Lys	Met	Met	Thr	Arg	Ala	Lys	Arg	Gln	Ile	Arg	Gln	Glu	Arg
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Ser	Lys	Glu	Lys	Ala	Lys	Ser	Arg	Asn	Glu	Asn	Cys	Leu	Asn	Arg	Lys
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Thr	Asn	Asp	Leu	Leu	Phe	Tyr	Ser	Cys	Glu	Arg	Met	Met	Met	Arg	Leu
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Pro	Gln	Gly	Leu	Met	Ala	Ser	Ala	Leu	Leu	Asp	Ile	Met	Arg	Ile	Pro
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385					390					395					400
Phe	Thr	Glu	Ala	Glu	Asp	Asp	Ile	Val	Arg	Leu	Thr	Ser	Cys	Leu	Leu
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Asn	Leu	Glu	Thr	Pro	Gly	Lys	His	Phe	Ser	Leu	Leu	Glu	Lys	Arg	Lys
			420					425					430		
Ile	Tyr	Asp	Ser	Tyr	Asn	Met	Ser	Gly	Asn	Arg	Lys	Glu	Ser	Lys	Arg
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Trp	Glu	Asp	Leu	Leu	Asn	Val	Leu	Lys	Gln	His	Thr	Asn	Asp	Glu	Asn
	450					455					460				

Gln	Thr	Leu	Ser	Met	Asn	Leu	Phe	Ser	His	Asp	Ser	Asp	Val	Leu	Val	465	470	475	480
Lys	Trp	Asn	Leu	Met	Val	Gly	His	His	Lys	Asn	Val	Cys	Arg	Leu	Thr	485	490		495
Gly	Thr	Gln	Phe	Lys	Asp	Ser	Glu	Thr	Phe	Leu	Lys	Ile	Gly	His	Val	500	505		510
Lys	Phe	Phe	Arg	Cys	Met	Asn	Ser	Asn	Ser	Ser	Gly	Glu	Asn	Gln	Ala	515	520		525
Asn	Glu	Leu	Gly	Gly	Phe	Ala	Ala	Lys	Arg	Arg	Thr	Lys	Pro	Asn	Thr	530	535		540
Ile	Tyr	Asn	Leu	Ala	Glu	Ser	Pro	Leu	Met	Leu	Ser	Pro	Glu	Ser	Thr	545	550		555
Leu	Leu	Ile	Met	Leu	Thr	Lys	Gly	Ser	Asp	Tyr	Asn	Ser	Ala	Ile	Val	565	570		575
Ser	Asn	Cys	Glu	Tyr	Asp	Thr	Trp	Val	Arg	Lys	Glu	Val	Ala	Val	Phe	580	585		590
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Glu	Gln	Glu	Ala	Arg	Lys	Asn	Asn	Lys	Asp	Cys	Asp	Asp	Ser	Val	Gly	610	615		620
Asn	Ile	Ser	Met	Gly	Asn	Leu	Ser	Lys	Ser	Asn	Cys	Arg	Lys	Cys	Asp	625	630		635
Lys	Lys	Leu	Val	Leu	Pro	Phe	Trp	Thr	Ile	Lys	Phe	Phe	Tyr	Leu	Ser	645	650		655
Gln	Ala	Ile	Asp	Phe	Val	Arg	Asp	Pro	Leu	Gln	Leu	Cys	Phe	Pro	Pro	660	665		670
Thr	His	Leu	Ile	Asp	Leu	Glu	Thr	Asp	Val	Ser	Leu	Lys	His	Ala	Leu	675	680		685
His	Arg	Ala	Val	Asn	Ala	Ala	Ala	Asn	Val	Met	Ser	Tyr	Leu	Thr	Met	690	695		700
Gly	Ser	Phe	Asn	Gln	Arg	Val	Phe	Gly	Thr	Ile	Thr	Thr	Leu	Ser	Asp	705	710		715
Ile	Ser	Ile	His	Leu	Ser	Gly	Ala	Asn	Asn	Asn	Glu	Ser	Lys	Asn	Thr	725	730		735
Gly	Ser	Asp	Val	Glu	Ser	Asp	Thr	Glu	Asp	Leu	Ile	Pro	Phe	Ser	Asn	740	745		750
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Ser	Lys	Val	Asn	Ala	Thr	Arg	Lys	Ser	Ala	Pro	Val	Thr	Lys	Lys	Leu	770	775		780
Ser	Ser	Ser	Val	Phe	Glu	Ser	Ile	Arg	Gly	Phe	Phe	Glu	Ser	His	Thr	785	790		795
Glu	Gly	Gly	Ile	Ile	Asn	Asp	Arg	Gly	Ile	Leu	Thr	Lys	Glu	Arg	Ile	805	810		815
Asp	Val	Phe	Gly	Asn	Asn	Leu	Asp	Thr	Asn	Pro	Glu	Ala	Leu	Gly	Glu	820	825		830
Glu	Asn	Gly	Gly	Gly	Gly	Gly	Ile	Val	Ser	Ser	Ile	Pro	Gly	Leu	Ser	835	840		845
Thr	Glu	Gln	Thr	Ser	Ile	Leu	Lys	Thr	Glu	Gln	Asn	Asn	Ser	Thr	Ser	850	855		860
Asp	Phe	Leu	Asp	Phe	Phe	Lys	Lys	Phe	Asn	Glu	Met	Asp	Asp	Val	Glu	865	870		875
Glu	Glu	Glu	Glu	Lys	Met	Glu	Glu	Gly	Glu	Lys	Glu	Glu	Glu	Glu	Ala	885	890		895
Asp	Leu	Glu	Thr	Asp	Asp	Trp	Leu	Asp	Glu	Ala	Arg	Lys	Ala	Phe	Glu	900	905		910
Tyr	Lys	Asp	Ser	Asp	Phe	Leu	Glu	Ala	Val	Thr	Ala	Ala	Thr	Asn	Glu	915	920		925
Met	Thr	Ser	Ser	Leu	Ala	Lys	Asn	Asn	Ile	Glu	Glu	Asp	Glu	His	Ser	930	935		940
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<212> PRT
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			20					25					30		
Leu	Glu	Val	Phe	Asn	Glu	Val	Ser	Asn	Ser	Ile	Glu	Thr	Val	Lys	Glu
		35					40					45			

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Glu Glu Asp Tyr Thr Val Leu Arg Ser Arg Asn Tyr Phe Pro Thr Glu
 50 55 60
 Ser Ile Thr Leu Tyr Lys Gln Gln Gln Glu Glu Glu Glu Ser Thr Pro
 65 70 75 80
 Ile Lys Lys Arg Lys Leu Ala Ser Gly Lys Ser Pro Arg Ser Leu Cys
 85 90 95
 Arg Glu Leu Arg Leu Leu Gln Ile Pro Ser Thr Thr Thr Phe Lys Ala
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 Val Cys Lys Asn Tyr Gly Ala His Gln
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 <212> PRT
 <213> SHRIMP

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 Gly Trp Thr Ala Ser Ser Thr Glu Cys Gln Val Pro Arg Val Asp Leu
 35 40 45
 Trp Val Gly Pro Met Ser Asp Tyr Thr Arg Asn Cys Trp Phe Gln Lys
 50 55 60
 Arg Thr Leu Thr Phe Val Cys Phe Trp Asn Arg Arg Phe Trp Arg Leu
 65 70 75 80
 Val Asp Pro Glu Met Arg Gly Tyr Asn Leu Phe Ser Leu Glu Asn
 85 90 95
 Phe Thr Leu Pro Leu Ser Gln Lys Leu Phe Lys Asn Phe Phe Arg Ala
 100 105 110
 Leu Gln Phe Arg Gly Trp Thr Ala Ser Ser Thr Glu Cys Gln Val Pro
 115 120 125
 Arg Val Asp Arg Trp Val Gly Pro Met Ser Asp Tyr Thr Arg Asn Val
 130 135 140

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Ile Ala Pro Glu Thr Tyr Ile Asn Phe Cys Val Phe Leu Glu Gln Ala
 145 150 155 160
 Phe Leu Glu Thr Gly Arg Pro Arg Asn Glu Arg Val Tyr Pro Ser Val
 165 170 175
 Phe Thr Arg Glu Phe Tyr Ser Ser Ser Ile Ser Lys Thr Phe Gln Lys
 180 185 190
 Phe Phe Arg Ala Leu Gln Phe Arg Gly Trp Thr Ala Ser Ser Thr Glu
 195 200 205
 Cys Gln Val Pro Arg Val Asp Leu Trp Val Gly Pro Met Ser Asp Tyr
 210 215 220
 Thr Arg Asn Val Ile Ala Pro Glu Ile Glu Glu Val Ser Tyr Gly His
 225 230 235 240
 Phe Trp Thr Arg Cys Phe Trp Thr Lys Ile Leu Leu Asp Gly Asn Pro
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 Leu Pro Leu Pro Pro Pro Phe Lys Lys Gly Pro Arg Val Tyr Asn Asp
 260 265 270
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 Leu
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 <212> PRT
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 35 40 45
 Phe Gln His Pro Val Leu Ala Glu Pro Thr His Asn Gln Ile Trp Thr
 50 55 60
 Pro Val Phe Pro Phe Ile Pro Asn Arg His His Leu Cys Pro Gln Ala
 65 70 75 80
 Val Tyr Ile Arg Arg Arg Gly Gln Ala Arg Ser Ile Ser Ser Leu Gln
 85 90 95
 Ala Ser Arg Arg Ala Thr Gln Gln Ala Leu Ser Leu Leu Leu Pro Arg
 100 105 110
 Arg Asp Leu Pro Ile Leu Lys Leu Gln Glu Trp Pro Leu Gln Pro Pro
 115 120 125

Pro His Gln Val Leu Thr Pro Cys Trp Thr Leu Ser Tyr Leu Val Leu
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 Arg Asn
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 <212> PRT
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 35 40 45
 Lys His Lys Phe Ser Leu Tyr Thr Leu Asp Phe Glu Ile Phe Tyr Val
 50 55 60
 Met Leu Asn Ile Leu Leu Val Glu Val Lys Asn Ile Leu Ser Pro Ile
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 <212> DNA
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<211> 931

<212> PRT

<213> SHRIMP

<400> 203

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Leu Ala Pro Phe Arg Asp Ile Ser Tyr Asp Ser Ser Lys Leu Asp Cys
35     40     45
Asp Ala Phe Ser Cys Ile Pro Ser Asp Ile Leu His Ser Asp Asn Glu
50     55     60
Lys Arg Val Gly Glu Cys Asn Phe Ala Glu His Thr Ser Val Ser Phe
65     70     75     80
Pro Val Lys Asn Pro Glu Gly Lys Thr Leu Arg His Phe Thr Ala Cys
85     90     95
Gly Pro Gly Cys Tyr Arg Arg Tyr Lys Gln Arg Asp Pro His Thr Gly
100    105    110
Leu Pro Val Arg Val Leu Met Gln Asp His Val Asp His Glu Thr Gly
115    120    125
Asn Lys Met Cys Glu Tyr Leu Asn Gln Ser Leu Val Met Trp Ala Ala
130    135    140
Val Pro Trp Ile Arg Pro Gly Asp Leu Thr Glu Gly Tyr Asn Thr Thr
145    150    155    160
His Val Pro Gly Phe Ala Phe Lys Glu Asp Asp Glu Arg Asp Ser Lys
165    170    175
Arg Val Lys Tyr Glu Asn Val Val Ile Ser Lys Ala Tyr Cys Asp Phe
180    185    190
Phe Lys Gln Tyr Tyr Asp Ala Asp Ser Gly Ser Cys Tyr Arg Ser Gly
195    200    205
Trp Met Lys Phe Val His Leu Met Phe Gly Gln Tyr Phe Thr Asn Leu
210    215    220
Ser Tyr Asn Leu Ala Asn Pro Lys Pro Tyr Asn Leu Thr Gly Asn Thr
225    230    235    240
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Lys Phe Asn Val Phe Pro Ser Glu Gln Thr Ser Ala Arg Gln Lys Ala
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Gly Thr Glu Lys Lys Ser Asp Arg Leu Met Arg Val Ala Asp Ala Val
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Met Asp Ala Ala Met Arg Leu Gln Val Met Gly Leu Asp Asp Ser Gln
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 Glu Asn Ile Thr Glu Asp Pro Lys His Pro Ala Pro Phe Val Asp Ile
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 625 630 635 640
 Leu Lys Lys Gln Val Leu Val Phe Arg Arg Glu Phe Ala Lys Ala Gly
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 740 745 750
 Gln Glu Gly Arg Arg Asp Asp Glu Thr Val Thr Lys Lys Met Arg Ser
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 770 775 780
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 785 790 795 800
 Ala Leu Lys Glu Glu Thr Arg Ser Asn Thr Thr Ser Asp Asn Leu Phe
 805 810 815
 Lys Lys Thr Val Ser Leu Ala Ser Met Ala Gly Ala Phe Leu Val Leu
 820 825 830
 Gly Ile Gly Val Leu Val Ala Ser His Ile Thr Leu Leu Arg Phe Thr

WO 01/38351

PCT/US00/28888

288

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Asn Ile Gly Leu Ala Phe Ala Phe Ala Gly Leu	Leu Ala Phe Ile Ala	
850	855	860
Leu Met Ser Ile Ser Tyr Ile Asn Met Asn Ala	Met Gly Val Val Asn	
865	870	875
Ser Asp Ala Ile Tyr Arg Ser Thr Ala Leu Val	Gly Asp Ile Lys Thr	
885	890	895
Asp Pro Arg Arg Val Gly Met Val Gln Arg His	Val Gly Val Gly Ala	
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Lys Tyr Asn Met Ile Thr Asp Phe Val Ser Pro	Met Leu Asp Glu Ile	
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930		

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 <212> DNA
 <213> SHRIMP

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<211> 1036

<212> PRT

<213> SHRIMP

<400> 205

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Phe Ile Lys Glu Met Gln Ser Tyr Ser Gly Cys Ile Pro Lys Asn Lys
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Tyr Thr Asn Val Gln Glu Ile Phe Glu Asp Gly Leu Ile Thr Phe Glu
65          70          75          80
Trp Arg Asp Gly Thr Lys Val His Arg Ser Val Ser Pro Ser Ser Pro
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Ile Pro Leu Ser Thr Lys Lys Ser Pro Arg Ser Ser Pro Ser Pro Pro
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Asp Asp Glu Glu Ile Tyr Glu Thr Asp Glu Asn Val Glu Asp Phe Ile
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Val Asp Asp Glu Glu Glu Glu Asn Glu Glu Gly Glu Asn Lys Tyr Val
165         170         175
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195         200         205
His Ala Val Ser Ala His Asp Tyr Thr Leu Ser Ala Leu Gln Gln Gln
210         215         220
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225         230         235         240
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245         250         255
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Phe Asp Val Asp Lys Ile Ala Gln Tyr Asn Gly Leu Val Glu Leu Asp
275         280         285
Ile Leu Pro Ile Val Ala Glu Tyr Ile Ile Asn Gly Leu Gly Leu Lys
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Val Trp Cys Gln Pro Lys Thr Ser Phe Glu Asn Asp Ala Val Glu Asp

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Ser	Asn	Phe	Arg	Val	Ser	Glu	Tyr	Ser	Arg	His	Phe	Asn	Glu	Phe	Ser
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Ser	Gln	Lys	Asn	Pro	Asn	Ile	Glu	Ile	Val	Ser	Lys	Leu	Asn	Ile	Glu
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Phe	Ser	Lys	Ile	Thr	Arg	Lys	Glu	Thr	Ile	Lys	Cys	Ser	Glu	Thr	Asp
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Pro	Asn	Ile	Ser	Ala	His	Gln	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn
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Thr	Ser	Val	Asn	Ile	Glu	Asp	Arg	Pro	Ile	Arg	Asn	Asn	Asn	Ile	Ser
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Cys	Thr	Asn	Asn	Cys	Thr	Asn	Gly	Asn	Tyr	Pro	Asp	Arg	Gly	Asn	Gln
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Asn	Ser	Lys	Val	Asp	Ser	Leu	Lys	Lys	Leu	Ser	Arg	Val	Leu	Ile	Pro
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Ala	Pro	Pro	Ser	Gly	Asn	Tyr	Thr	Ser	Lys	Phe	Cys	Asp	Arg	Ser	Ser
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Phe	Ser	Ser	Asp	Ser	Phe	Glu	Lys	Thr	Lys	Leu	Val	Leu	Tyr	Gly	Lys
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 915 920 925
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<210> 207
 <211> 361
 <212> PRT
 <213> SHRIMP

WO 01/38351

PCT/US00/28888

292

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<400> 207

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			20					25					30		
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	50					55					60				
Leu	Lys	Lys	Asn	Val	Lys	Ser	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val
65					70					75					80
His	Leu	Asp	Val	Lys	Ser	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val	His
			85					90					95		
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			100					105					110		
Asp	Val	Lys	Ser	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val	His	Leu	Asp
		115					120					125			
Val	Arg	Gly	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val	Arg	Leu	Asp	Val
	130					135					140				
Arg	Gly	Ala	Lys	Gln	Asn	Pro	Trp	Arg	Lys	Asn	Leu	Cys	Leu	Leu	Lys
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				165					170					175	
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			180					185					190		
Val	Arg	Gly	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val	His	Leu	Asp	Val
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	210					215					220				
Lys	Asn	Val	Lys	Ser	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val	Leu	Leu
225					230					235					240
Asp	Val	Arg	Gly	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val	Leu	Leu	Asp
				245					250					255	
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			260					265					270		
Arg	Gly	Ala	Lys	Gln	Asn	Pro	Trp	Arg	Lys	Asn	Leu	Cys	Leu	Leu	Lys
		275					280					285			
Lys	Asn	Val	Lys	Ser	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val	Leu	Leu
	290					295					300				
Asp	Val	Arg	Gly	Ala	Lys	Gln	Leu	Pro	His	Leu	Lys	Val	His	Leu	Asp
305					310					315					320
Val	Arg	Gly	Ala	Lys	Gln	Gln	Gln	Gln	Leu	Cys	Leu	Pro	Leu	Lys	Thr
				325					330					335	
Ile	Ser	Thr	Ser	Phe	Thr	His	Leu	Leu	Leu	Cys	Leu	Tyr	Met	Glu	Tyr
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Gly	Lys	His	Gln	Asn	Leu	Gln	Val	Xaa							
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<210> 208
 <211> 816
 <212> DNA
 <213> SHRIMP

<400> 208

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<210> 209
 <211> 269
 <212> PRT
 <213> SHRIMP

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Asp Ser Arg Asn Lys Gly Glu Asp Gly Cys Cys Ser Phe Cys Gly Arg
 35          40          45
Arg Gly Thr Gly Glu Ser Asn Thr Ala Cys Leu Glu Gln Leu Ile Asp
 50          55          60
Val Cys Ser Phe Ile Gly Thr Val Ser Ser Ile Gly Thr Ile Ile Asn
 65          70          75          80
Ser Asn Leu Ser Thr Ser Cys Ser Arg Leu Gln Lys Thr Ser Asp Ser
 85          90          95
Tyr Ala Ala Leu Ser His Ser Ser Phe Leu Asp Val Val Tyr Pro Ser
100          105          110
Leu Lys Lys Thr Thr Glu Asp Val Leu Pro His Ser Leu Arg Ala Ile
115          120          125
Trp Asn Lys Gln Leu Pro Lys Leu Tyr Glu Lys Thr Leu Gln Pro Ile
130          135          140
Glu Glu Glu Asp Ile Gly Tyr Lys Asp Tyr Val Val Ser Ile Glu Asp
145          150          155          160
Asp Asp Asn Val Asp Asp Gly Asp Gln Gln Glu Gln Met Ile Ile Asp
165          170          175
Glu Glu Ser Tyr Lys Thr Ile Gly Glu Lys Ser Thr Ile Glu Leu Ile
180          185          190
Gly Met Tyr Asn Asn Asn Lys Phe Gly Asn Glu Phe Ile Arg Ile Pro
195          200          205
Leu Arg Glu Thr Ala Leu His Ala Gln Ser Leu Arg Tyr Asp Thr Glu
210          215          220
Ala Lys Phe Val Asn His Lys Asp Ser Ile Pro Leu Phe Tyr Glu Asn
225          230          235          240
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<210> 210
 <211> 3813
 <212> DNA
 <213> SHRIMP

<400> 210

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gatatcatat	ccttagtgga	aagtgtatat	gaacctgtat	tttctaaatc	acttaaacct	300
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<210> 211

<211> 1264

<212> PRT

<213> SHRIMP

<400> 211

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			20					25					30		
Leu	Lys	Lys	Ser	Asn	Asn	Leu	Ser	Ile	Ala	Arg	Pro	Pro	Ser	Ile	Glu
		35				40						45			
Ser	Phe	Ser	Ala	Ser	Val	Glu	Lys	Ile	Phe	Arg	Glu	Trp	Asn	Glu	Ser
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Gly	Gly	Glu	Lys	Ile	Phe	Asp	Ile	Ser	Gln	Asn	Glu	Glu	Trp	Met	
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Asp	Ile	Ile	Ser	Leu	Val	Glu	Ser	Val	Tyr	Glu	Pro	Val	Phe	Ser	Lys
			85						90					95	
Ser	Leu	Lys	Pro	Asp	Lys	Leu	Ala	Asp	Lys	Thr	Cys	Leu	Thr	Ala	Ala
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Ala	Phe	Ala	Ala	Ser	Ala	Val	Asp	Glu	Lys	Leu	Thr	Ile	Leu	Ser	Gly
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Ser	Asp	Gly	Ser	Val	Leu	Gln	Arg	Thr	Thr	Lys	Val	Met	Lys	Lys	Asp
	130					135					140				
Pro	Lys	Lys	Ile	Ala	Glu	Ser	Leu	Leu	Asn	Asn	Glu	Lys	Trp	Thr	Ser
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Ile	Leu	Leu	Asp	Arg	Leu	Lys	Thr	Ala	Lys	Lys	Leu	Leu	Ser	Arg	Arg
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Gly	Ala	Leu	Lys	Ser	Ala	Glu	Arg	Val	Glu	Val	Leu	His	Arg	Leu	Asn
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Lys	Leu	Lys	Glu	Ala	Pro	Leu	Pro	His	His	Pro	Ser	Leu	Phe	Asp	Asn
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Phe	Ser	Gly	Gly	Lys	Thr	Ser	Ala	Val	Ser	Ala	Gly	Thr	Val	Ile	Ala
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Ser	Asp	Met	His	Phe	Lys	Leu	Val	Glu	His	Ile	Phe	Lys	Val	Ser	Phe
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Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Lys	Lys	His	Ser	Ile	Ser	Arg	Phe
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Phe	Asn	Met	Glu	Asp	Leu	Pro	Phe	Arg	Pro	Phe	Ala	Val	Pro	Ser	Thr
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Pro	Gln	Leu	Ser	Phe	Asp	Tyr	Gly	Glu	Phe	Leu	Cys	Tyr	Cys	Ile	Phe
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Asn	Ser	Ser	Met	Ile	Ser	Phe	Asp	Ser	Gln	Thr	Leu	Ser	Gly	Val	Tyr
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Ala	Asp	Leu	Ala	Val	Arg	Ser	Met	Ala	Glu	Phe	Ile	Arg	Thr	Glu	Ala
			420					425					430		
His	Lys	Ala	Leu	Thr	Ala	Glu	Glu	Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu
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Glu	Ala	Glu	Glu	Glu	Ala	Met	Asp	Gln	Glu	Pro	Ala	Glu	Val	Asp	Phe
	450					455				460					
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			485					490						495	
Lys	Asn	Val	Leu	Thr	Asp	Asp	Thr	Val	Ser	Gly	Thr	Asp	Thr	Asp	Asn
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Phe	Gly	Ser	Ser	Gly	Glu	Phe	Glu	Ala	Leu	Ser	Ser	His	Leu	Phe	Leu
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Lys	Thr	Asn	Gln	Pro	Pro	Pro	Pro	Ala	Arg	Ser	Ala	Lys	Ile	Thr	Val
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Glu	Gly	Val	Lys	Gly	Phe	Phe	Ser	Gly	Phe	Arg	Asp	Ile	Thr	Arg	Ala
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Phe	Ser	Glu	Gly	Leu	Ala	Glu	Ser	Leu	Arg	Ser	Asp	Ala	Asn	Leu	Gly
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Leu	Glu	Phe	Ser	Glu	Asp	Ala	Lys	Thr	Val	Val	Phe	Lys	Asn	Asp	Thr
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Ser	Phe	Ser	Ser	Phe	Ala	Arg	Asp	Met	Gly	Val	Gln	Val	Ser	Ala	Asp
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Leu	Asp	Ala	Glu	Phe	Ala	Ala	Glu	Met	Arg	Glu	Thr	Tyr	Pro	Asp	Ala
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Ala	Leu	Glu	Gln	Asn	Leu	Lys	Asp	Leu	Asp	Lys	Phe	Glu	Glu	Thr	Ile
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Pro	Glu	Ser	Gln	Val	Lys	Lys	Leu	Lys	Lys	Ile	Asp	Ser	Tyr	Leu	Thr
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Glu	Asn	Pro	Glu	Arg	Ala	Gly	Lys	Glu	Ile	Asn	Asp	Thr	Glu	Leu	Ser

				885					890					895			
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PCT/US00/28888

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 Glu Lys Asn Pro Ser Ala Ile Pro Ala Asn Glu Leu Asn Arg Tyr Trp
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 Thr Lys Thr Asn Val Leu Cys Asn Pro Leu Phe Lys Leu Glu Asp His
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 Ile Thr Arg Asp Glu Asp Thr Gly Thr Ile Thr Leu Lys Phe Lys Met
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 Tyr Ile Asp Asp Lys Asn Gly Gln Ser Ala Val Leu Met Leu Ala Leu
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 Asp Ser Phe Val Ser Leu Ala Ser Phe Ser His Gly Ala Asp Leu Val
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Ile Ser Phe Gln Glu Met Asp Asp Phe Leu Ala Asp Tyr Ala Lys Thr
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Ser Pro Thr Asp Arg Lys Lys Arg Ile Leu Val Glu Arg Pro Gln Asp
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Ala	Ala	Phe	Ser	Ala	Pro	Val	Arg	Glu	Glu	Glu	Glu	Glu	Lys	Lys	Ser
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Ser	Ile	Val	Val	Pro	Asp	Pro	Ala	Ala	Ala	Leu	Leu	Cys	Ser	Ile	Asn
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Asn	Pro	Gly	Ala	Cys	Glu	Met	Cys	Ser	Ser						
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<210>	222
<211>	222
<212>	DNA
<213>	SHRIMP

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atacatagtc agataaaact tattccttat tcaaatatgc acgtatatat agcagggtgtg 180
tacacatttc atgaaaaaaa ggggttaaca tatcaacaat at 222
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<210> 223
<211> 74
<212> PRT
<213> SHRIMP
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[illegible]

<210>	224
<211>	1848
<212>	DNA
<213>	SHRIMP

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gtcatgggtg	tttatgaagc	tatcgaatct	ataagacaaa	gcgaattgtc	cgaagacaca	180
tttgttgtac	atgtgaagaa	agataaacaa	ctcaaatctc	caagagggtt	aaaaagatta	240
caagaattgg	tagaagatga	ctcttttaaga	attgaacgga	taagttgtgc	ccctcctgaa	300
cctggacatt	tattcaaaga	tgatgctggg	cacgttactg	acgaggtaatg	gcttgcaacg	360
caagaagaag	acgtgcgtaa	aatcaataca	atagtcaagg	aaaaattaaa	acgaaaagac	420
aaggacttta	aattcagtca	attatacagg	tacatgagca	atagtctttc	tgaagcagta	480
gaaaaaaaaa	acgattgtat	gataataaagt	tccgatttct	taatcggttt	aggtttcagt	540
acaatgaacg	tcacgcacgc	tttaaagtca	atggagagaa	ctatgcagaa	acatggtttc	600
aaggatatag	tgtgtccatt	ggttgaaatt	tgtcaccgta	cccattacaa	aggagaatat	660
atagccaatc	ctattttcaa	gagccattct	tcacattgct	tgtattgtcc	cttgtttatg	720
gtggcgggcg	tttttgcaag	gagcgcacac	ccttctgctg	caagcattga	aatgtacctt	780
tcgacactag	cctacgctgt	tatcttatac	agtgatgaaa	agcaacgcca	gatacgcgaa	840
gagttggcta	ggaaaaattt	acaaaataaaa	gaggaactag	aaaaccaggt	cgaaaagacc	900
acaaaagttg	aaaaggaact	agaaacacaa	gtagttaaga	ccacaaaagt	tgaaaaggaa	960
ctagaaacac	aagttagtaa	gaaagaggag	tacataaaact	cgtatatcga	aactgaacaa	1020
cttttcaaag	tctctgagga	acaaaaagaa	tctctcagaa	atgtacacaa	qaaatcttcc	1080

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314

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ctcatcatgg ccgtgactgg ctgtgacgca cctatcgctt gcaacgacag tatcaaacac 1320
caaaacaagt tcaaggtatt aaaatgtaac cgatcaagta tagttttcca gaccctcca 1380
agtgatgaag atttgaaggg tattgtacaa aaagtgcacag gttctgatata ccgaatcttt 1440
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cttgatgaag aaaatatgac ccaatttgaa attgaacaac aaaggaagct ccattccatg 1560
atggagaaca catcaaaaat tgtcactagg tacaacaagg aaagacattt gaccacaaag 1620
gaagctcgta cgagaaaaca gaccgaaaag tggtttgaga aggtaaagaa gagggaggaa 1680
caaaagaagc gagaaaatgg agaacagtct accagtgaac aggagcaaag gggagtaaaa 1740
aggacctggg aaaacgacaa tgaatttgat agcgacgtag aagaagaaga agatggaaac 1800
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<210> 225

<211> 611

<212> PRT

<213> SHRIMP

<400> 225

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Met Glu Tyr Ile Gly Glu Lys Asn Asn Asn Pro Val Ser Asn Glu Ser
 1          5          10          15
Val Ser Glu Lys Glu Leu Lys Leu Arg Ser Ser Phe Leu Met Ile Gly
 20          25          30
Lys Lys Thr Ser Lys Tyr Glu Gln Val Met Gly Val Tyr Glu Ala Ile
 35          40          45
Glu Ser Ile Arg Gln Ser Glu Leu Ser Glu Asp Thr Phe Val Val His
 50          55          60
Val Lys Lys Asp Lys Gln Leu Lys Phe Arg Leu Lys Arg Leu Gln Glu
 65          70          75          80
Leu Val Glu Asp Asp Ser Leu Arg Ile Glu Arg Ile Ser Cys Ala Pro
 85          90          95
Pro Glu Pro Gly His Leu Phe Lys Asp Asp Ala Gly His Val Thr Asp
100          105          110
Glu Glu Trp Leu Ala Thr Gln Glu Glu Asp Val Arg Lys Ile Asn Thr
115          120          125
Ile Val Lys Glu Lys Leu Lys Arg Lys Asp Lys Asp Phe Lys Phe Ser
130          135          140
Gln Leu Tyr Arg Tyr Met Ser Asn Ser Leu Ser Glu Ala Val Glu Lys
145          150          155          160
Lys His Asp Cys Met Ile Ile Ser Ser Asp Phe Leu Ile Gly Leu Gly
165          170          175
Phe Ser Thr Met Asn Val Thr His Ala Leu Lys Ser Met Glu Arg Thr
180          185          190
Met Gln Lys His Gly Phe Lys Asp Met Met Val Pro Leu Val Glu Ile
195          200          205
Cys His Arg Thr His Tyr Lys Gly Glu Tyr Ile Ala Asn Pro Ile Phe
210          215          220
Lys Ser His Ser Ser His Cys Leu Ile Val Pro Leu Phe Met Val Ala
225          230          235          240
Gly Val Phe Ala Arg Ser Ala His Pro Ser Ala Ala Ser Ile Glu Met
245          250          255
Tyr Leu Ser Thr Leu Ala Tyr Ala Val Ile Lys Asp Glu Lys Gln Arg
260          265          270
Gln Ile Arg Glu Glu Leu Ala Arg Lys Asn Leu Gln Ile Lys Glu Glu
275          280          285
Leu Glu Asn Gln Val Glu Lys Thr Thr Lys Val Glu Lys Glu Leu Glu
290          295          300
Thr Gln Val Val Lys Thr Thr Lys Val Glu Lys Glu Leu Glu Thr Gln
305          310          315          320
Val Val Lys Lys Glu Glu Tyr Lys Asn Ser Tyr Ile Glu Thr Glu Gln

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<400> 226						
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gttttcattg	tacaatttaa	ggaaaataaa	cacattactt	ttgaaggggg	actgaaagaa	240
ttaagagagc	tcacaggggg	caattccctc	aagatagaat	cattattatc	ctctattaag	300
cctgagaaaag	gacacgttat	acttaaaaac	acgtctacaa	ctactgatga	cgagtggctt	360
gcttctcaag	acaaagacgt	acaggaagta	aataagctcg	taaaggaaaa	gacacggatg	420
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atacctttcg	gggaaaagca	acgttttgtt	gttagcacag	attttttgat	tgtgtctcgg	540
tttagtgctg	atgatgtcat	ggaaaaatta	atagcgatag	agggaaatat	tcgggaaaagt	600
ggtctgaaat	atacatgggt	gcctgtggcc	gaagtgtgcc	atctcaaaaa	atacaagggt	660
gatattgttg	taaaccocat	tttcaagagt	tatcattccc	attgcctagt	tattccactg	720
gtgtatctag	ggtacatgtt	ttcccgtaat	gttcaacccc	catctctaga	agtggagacg	780
tatctttctg	cgttagcgtt	tgctattgat	ttgtacggca	gggaagaaat	gcgcaagtct	840
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316

<210> 227
 <211> 290
 <212> PRT
 <213> SHRIMP

<400> 227

Met	Glu	Tyr	Ile	Gly	Glu	Gln	Lys	Leu	Ile	Asn	Leu	Leu	Asp	Glu	Thr
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Pro	Glu	Glu	Asp	Glu	Leu	Gln	Leu	Arg	Ser	Ser	Phe	Leu	Met	Ile	Gly
			20					25					30		
Glu	Lys	Gln	Tyr	Glu	Lys	Tyr	Glu	Glu	Val	Met	Ser	Thr	Phe	Glu	Ala
		35					40					45			
Val	Glu	Thr	Ile	Arg	Lys	Ser	Glu	Phe	Arg	Asp	Gly	Val	Phe	Ile	Val
	50					55				60					
Gln	Leu	Lys	Glu	Asn	Lys	His	Ile	Thr	Phe	Glu	Gly	Gly	Leu	Lys	Glu
65				70						75				80	
Leu	Arg	Glu	Leu	Thr	Gly	Asp	Asn	Ser	Leu	Lys	Ile	Glu	Ser	Leu	Leu
				85				90					95		
Ser	Ser	Ile	Lys	Pro	Glu	Lys	Gly	His	Val	Ile	Leu	Lys	Asn	Thr	Ser
			100					105					110		
Thr	Thr	Thr	Asp	Asp	Glu	Trp	Leu	Ala	Ser	Gln	Asp	Lys	Asp	Val	Gln
		115					120					125			
Glu	Val	Asn	Lys	Leu	Val	Lys	Glu	Lys	Thr	Arg	Met	Leu	Phe	Arg	Gly
	130					135					140				
Phe	Tyr	Phe	Ser	Pro	Tyr	Tyr	Ile	Thr	Lys	Ser	Leu	Pro	Gln	Ile	Pro
145					150					155					160
Phe	Gly	Glu	Lys	Glu	Arg	Phe	Val	Val	Ser	Thr	Asp	Phe	Leu	Ile	Gly
				165					170					175	
Leu	Gly	Phe	Ser	Ala	Asp	Asp	Val	Met	Glu	Lys	Leu	Ile	Ala	Ile	Glu
			180					185					190		
Gly	Asn	Met	Arg	Lys	Ser	Gly	Leu	Lys	Tyr	Thr	Trp	Val	Pro	Val	Ala
	195						200					205			
Glu	Val	Cys	His	Leu	Lys	Lys	Tyr	Lys	Gly	Asp	Ile	Val	Val	Asn	Pro
	210					215					220				
Ile	Phe	Lys	Ser	Tyr	His	Ser	His	Cys	Leu	Val	Ile	Pro	Leu	Val	Tyr
225					230					235					240
Leu	Gly	Tyr	Met	Phe	Ser	Arg	Asn	Val	Gln	Pro	Pro	Ser	Leu	Glu	Val
				245					250					255	
Glu	Thr	Tyr	Leu	Leu	Ala	Phe	Ala	Ile	Asp	Leu	Tyr	Gly	Arg	Glu	Glu
			260					265					270		
Met	Arg	Lys	Ser	Cys	Met	Arg	Leu	Cys	Glu	Asp	Ile	Ser	Glu	Val	Lys
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Arg	Gly														
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<210> 228
 <211> 2769
 <212> DNA
 <213> SHRIMP

<400> 228

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agtcaca	ca	cgaaa	actgt	ggaaga	agt	gtaggag	agg	aagaaga	aca	gcagcag	cag	240
actcctc	cag	aaatcac	acc	cgccgag	aag	aagcag	caat	ctcttca	aga	actggac	gct	300
cttatgg	gca	aggtgcc	agc	tcattct	tgac	gtgagt	gttc	tgcccaa	atc	tgttgct	gaa	360
tttctgg	aga	atgacga	aga	tgaggac	gaa	gaattgg	aga	agaata	agaa	ggcgcag	aaa	420
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<210> 229

<211> 922

<212> PRT

<213> SHRIMP

<400> 229

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 20          25          30
Ser Ala Lys Lys Pro Thr Pro Ser Lys Ala Lys Phe Ala Ala Gly Arg
 35          40          45
Arg Met Val Ser Lys Gln Arg Arg Asn Thr Ile Arg Ser Pro His Thr
 50          55          60
Glu Thr Val Glu Glu Val Val Gly Glu Glu Glu Glu Gln Gln Gln Gln
 65          70          75          80
Thr Pro Pro Glu Ile Thr Pro Ala Glu Lys Lys Gln Gln Ser Leu Gln
 85          90          95
Glu Leu Asp Ala Leu Met Gly Lys Val Pro Ala His Leu Asp Val Ser
100          105          110
Val Leu Ala Lys Ser Val Ala Glu Phe Leu Glu Asn Asp Glu Asp Glu
115          120          125

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Asp	Glu	Glu	Leu	Glu	Lys	Asn	Lys	Lys	Ala	Gln	Lys	Ser	Val	Leu	Phe
130						135					140				
Asn	Ser	Val	Met	Asn	Ser	Gly	Arg	Thr	Glu	Leu	Ser	Pro	Ser	Thr	Phe
145					150					155					160
Cys	Asp	Gly	Cys	Val	Ser	Lys	Val	Lys	Ser	Ala	Phe	Glu	Gly	Lys	Asp
				165					170					175	
Leu	Val	Ser	Asn	Ile	Val	Lys	Val	Glu	Gly	Glu	Ala	Val	Lys	Lys	Thr
			180					185					190		
Ala	Ile	Ala	Thr	Asp	Thr	Thr	Lys	Leu	Ala	Asn	Leu	Phe	Leu	Gly	Cys
		195					200					205			
Met	Asn	Leu	Gln	Phe	His	Glu	His	Val	Thr	Ile	Glu	Thr	Leu	Asn	Lys
210						215					220				
Lys	Ala	Leu	Asp	Lys	Gly	Gly	Pro	Leu	Phe	Thr	Leu	Lys	Leu	Ser	Asp
225					230					235					240
Ala	Val	Tyr	Val	Asp	Glu	Met	Asp	Leu	Glu	Lys	Lys	Arg	Gln	Ile	Phe
				245					250					255	
Gly	Ser	Asn	Gly	Asp	Lys	Ser	Leu	Phe	Lys	Glu	Leu	Gly	Gly	Asn	Tyr
			260					265					270		
Ile	Asp	Ser	Ala	Ile	Lys	Ser	Thr	Gly	Leu	Val	Met	Ser	Thr	Pro	Ser
		275					280					285			
Ser	Ser	Ser	Thr	Lys	Lys	Ala	Gly	Thr	His	Phe	Lys	Thr	Thr	Asn	Gln
290						295					300				
Ile	Val	Glu	Glu	Ser	Val	Thr	Glu	Ser	Met	Arg	Asn	Gly	Cys	Cys	Cys
305					310					315					320
Phe	Lys	Asn	Asp	Lys	Trp	Leu	Ala	Lys	Arg	Glu	Ser	Asn	Leu	Lys	Ser
				325					330					335	
Leu	Asn	Asn	Thr	Val	Phe	Gly	Glu	Glu	Asp	Asp	Glu	Lys	Ser	Ala	Tyr
			340					345					350		
Ala	Tyr	Ser	Asp	Ser	Glu	Asp	Glu	Asp	Glu	Asp	Glu	Asn	Glu	Glu	Glu
		355					360					365			
Val	Asp	Tyr	Asp	Tyr	Asn	Asn	Glu	Thr	Ile	Glu	Ser	Ser	Val	Gly	Asn
	370					375					380				
Val	Ile	Lys	Asn	Leu	Ile	Arg	Lys	Thr	Ile	Gly	Leu	Ser	Asp	Val	Glu
385					390					395					400
Glu	Glu	Lys	Glu	Glu	Gly	Glu	Gln	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ser
				405					410					415	
Asp	Asp	Asp	Asp	Asp	Asp	Ala	Ser	Ser	Val	Cys	Ser	Ser	Ser	Ser	Ser
			420					425					430		
Ser	Ser	Ser	Val	Thr	Val	Val	Ala	Ala	Ala	Glu	Glu	Glu	Glu	Glu	Glu
		435					440					445			
Asp	Glu	Glu	Asp	Lys	Asp	Lys	Asp	Thr	Ala	Thr	Val	Val	Glu	Asp	Glu
	450					455					460				
Asp	Asp	Lys	Glu	Ser	Val	Ile	Ser	Ser	Ser	Ser	Glu	Asp	Ser	Glu	Glu
465					470					475					480
Asp	Glu	Asp	Asp	Asp	Gly	Ala	Thr	Ser	Gln	Cys	Ser	Glu	Val	Val	Phe
				485					490					495	
Gly	Asp	Val	Thr	Glu	Cys	Glu	Phe	Asp	Glu	Ser	Asp	Gly	Asn	Pro	Leu
			500					505					510		
Tyr	Leu	Ala	Ser	Asp	Asn	Ser	Phe	Arg	Pro	Ser	Ala	Ser	Val	Thr	Lys
		515					520					525			
Tyr	Pro	Gln	Ser	Glu	Glu	Glu	Met	Asp	Val	Ser	Leu	Leu	Ser	Lys	Asn
	530					535					540				
Arg	Ser	Thr	Pro	Val	Cys	Leu	Ser	Leu	Cys	Arg	His	Ser	Ser	Gly	Cys
545					550					555					560
Ile	Thr	Asn	Ser	Phe	Asn	Met	Ser	Thr	Ile	Leu	Lys	Ser	Leu	Lys	Leu
				565					570					575	
Phe	Pro	Ala	Gly	Thr	Glu	Ala	Ala	Glu	Asp	Cys	Val	His	Ile	Glu	Ser
			580					585					590		
Thr	Lys	Lys	Lys	Asp	Glu	Asp	Glu	Asp	Glu	Glu	Asp	Gln	Gly	Leu	Asp
		595					600					605			
Leu	Gln	Asn	Ser	Gln	Tyr	Tyr	Ser	Val	Leu	Val	Asp	Val	Asp	Asn	Leu

610		615		620
Ile Ile Phe Ser Met Gly Ser Thr Thr Tyr Glu Ser Ser Met Val Glu				
625		630		635
Val Asp Tyr Asp Lys Ser Phe Trp Ser Ser Phe Asp Lys Ser Val Lys				
	645		650	655
Pro Tyr Cys Glu Ser Lys Lys Ser Ala Leu Ile Asn Ala Leu Cys Glu				
	660		665	670
Asp Asn Val Thr Ala Lys Val Tyr Ala Thr Val His Thr Leu Ala Ile				
	675		680	685
Pro Phe Cys Glu Ser Met Pro Ile Asn His Ile Asn Asn Thr Thr Pro				
	690		695	700
Tyr Gly Ser Tyr Lys Thr Phe Arg Ile Ser Leu Pro Gly Asn Phe Ser				
705		710		715
Gly Gln His Asn Asp Ile Asn Asn Asn Trp Arg Ser Asp Met Tyr Thr				
	725		730	735
Lys Met Val Glu Asn Leu Leu Lys Arg Glu Val Val Glu Asn Lys Thr				
	740		745	750
His Ser Arg Arg Tyr Val Arg Asn Leu Ile Val Asp Gly Gly Val Gly				
	755		760	765
Glu Asn Ser Gly Asn Tyr Leu Lys Val His Glu Asn Asn Glu Asp Ile				
	770		775	780
Phe Gly Ser Ile Glu Ala Asn Ser Met Ser Ala Lys Thr Ala Ala Ala				
785		790		795
Ala Phe Lys Asn Val Ala Lys Lys Cys Asp Leu Ile Gln Thr Thr Thr				
	805		810	815
Asn Asp Ile Leu Thr Gly Pro Phe Lys Gln Tyr Leu Ile Asp Tyr Lys				
	820		825	830
Tyr Asn Ser Ala Arg Lys Asn Ile Ile Met Glu Pro Cys Glu Gly Asp				
	835		840	845
Glu Thr Thr Ala His Glu Met Lys Arg Ala Gln Asp Ala Tyr Lys Gln				
	850		855	860
Ala Leu His Arg Ala Lys Ile Thr Ala Ser Ser Ile Ser Leu Arg Gly				
865		870		875
Ile Trp His Glu Met Ile Thr Arg Asp Met Asn Thr Thr Tyr Asn Ser				
	885		890	895
Met Phe Met Tyr Ile Pro Asp Phe Tyr Lys Tyr Val Gln Val Ser Pro				
	900		905	910
Val Asn Val Ser Pro Leu Tyr Met Leu Asp				
	915		920	

<210> 230

<211> 846

<212> DNA

<213> SHRIMP

<400> 230

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320

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846

<210> 231
 <211> 281
 <212> PRT
 <213> SHRIMP

<400> 231

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Ile	Asn	Lys	Asn	Gln	Asp	Val	Pro	Pro	Glu	Leu	Ala	Asn	Ala	Ser	Ser
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Cys	Cys	Leu	Leu	Glu	Thr	Ile	Asn	Ser	Phe	Asn	Gly	Ser	Cys	Ser	Ser
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Leu	Gln	Met	Lys	Trp	Val	Glu	Gln	Asn	Glu	Leu	Asp	Ala	Glu	Ser	Pro
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 <211> 1470
 <212> DNA
 <213> SHRIMP

<400> 232

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<210> 233

<211> 487

<212> PRT

<213> SHRIMP

<400> 233

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35     40     45
Asp Val Arg Phe Thr Gly Arg Lys Ser Met Asp Glu Leu Ala Arg Cys
50     55     60
Leu Tyr Asn Cys Asp Gly Glu Tyr Thr Thr Leu Arg Leu Val Gly Ser
65     70     75     80
Ser Ala Gly Asn Ile Ile Val Tyr Ser Leu Ala Phe Ile Met Gly Ile
85     90     95
Arg Gly Glu Cys Cys Gly Phe Asn Val Asn Asn Arg Leu Arg Met Gly
100    105    110
Lys Ile Ile Asp Arg Glu Leu Phe Tyr Lys Ile Thr Gln Phe Pro Glu
115    120    125
Thr Val Lys Cys Thr Cys Asp Gly Val Arg Ala Ile Cys Asp Leu Phe
130    135    140
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165    170    175
Tyr Pro Gly Thr Lys Phe Asn Lys Arg His Lys Leu Ser Thr Lys Ile
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225    230    235    240
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245    250    255
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 325 330 335
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 340 345 350
 Leu Lys Leu Arg Asn Asn Lys Ser Leu Ser Lys Leu Ala Lys Trp Lys
 355 360 365
 Trp Asn Gly Met Val Ser Thr His Asp Asn Phe Asp Ser Asn Asp Tyr
 370 375 380
 Val Ile Glu His Lys Arg Gln Leu Ala Ala Asp Ile Met Ser Asp Ser
 385 390 395 400
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 405 410 415
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 Phe Glu Leu Ser Pro Met Gly Lys His Leu Phe Pro Leu Glu Glu Val
 435 440 445
 Cys Gly Phe Tyr Glu Ala Ser Leu Pro Leu Ile Thr Pro Trp Gln Leu
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<210> 234

<211> 4698

<212> DNA

<213> SHRIMP

<400> 234

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<210> 235

<211> 1551

<212> PRT

<213> SHRIMP

<400> 235

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Thr	Ile	Glu	Glu	Ile	Ser	Thr	Lys	Ser	Leu	Asn	Ala	Leu	Val	Glu	Lys
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210

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		595					600					605			
Thr	Asn	Ile	Lys	Gly	Lys	Tyr	Glu	Gly	Gln	Lys	Lys	Ser	Leu	Tyr	Gly
	610					615					620				
Asn	Lys	His	Ser	Ser	Cys	Phe	Lys	Thr	Asn	Thr	Glu	Ser	Asn	Val	Asn
625					630					635					640
Asn	Ala	Leu	Phe	Ala	Trp	Val	Lys	Ser	Lys	Leu	His	Ser	Gly	Thr	Val
				645					650					655	
Ile	Pro	Asn	Val	Phe	Ser	Phe	Lys	Met	Ala	Ser	Glu	Lys	Pro	Ser	Lys
			660					665					670		
Met	Lys	Arg	Lys	Arg	Thr	Ser	Ser	Ala	Ser	Ser	Ser	Asn	Asp	Glu	His
		675					680					685			
Gln	Glu	Pro	Ser	Thr	Lys	Met	Met	Lys	Asn	Asp	Glu	Gly	Glu	Lys	Val
	690					695					700				
Ala	Gln	Glu	Ser	Ser	Ser	Pro	Ser	Ser	Ser	Ser	Thr	Pro	Glu	Gln	Gln
705					710					715					720
Gln	Gln	Ala	Gly	His	Asp	Lys	Glu	Thr	Ile	Asn	Leu	Ile	Pro	Leu	Ser
				725					730					735	
Phe	Ile	Lys	Met	Pro	Arg	Ser	Asn	Val	Asn	Gly	Ser	Ala	Ser	Tyr	Leu
			740					745					750		
Ser	Glu	Ile	Phe	Gly	Gln	Arg	Leu	Cys	Gly	Leu	Ser	Asp	Ala	Ser	Ser
		755					760					765			
Thr	Phe	Lys	Arg	Met	Cys	Lys	Thr	Phe	Glu	Asp	Leu	Glu	Asn	Glu	Ile
		770				775					780				
Met	Arg	Ser	Ser	Phe	Thr	Arg	Leu	Thr	Arg	Tyr	Glu	Arg	Glu	Val	Thr
785					790					795					800
Arg	Leu	Tyr	Glu	Lys	Cys	Arg	Ser	Gln	Ala	Val	Asp	Ile	Glu	Glu	Asn
				805					810					815	
Glu	Met	Asp	Val	Leu	Ser	His	Gln	Gly	Glu	Leu	Phe	Ala	Glu	Phe	Leu

			820				825				830				
Glu	Asp	Pro	Ile	Ala	Tyr	Phe	Glu	Glu	Val	Leu	Glu	Asn	Ile	Lys	Ser
835							840				845				
Trp	Ser	Leu	Glu	Asn	Val	Asn	Glu	Thr	Pro	Lys	Arg	Lys	Asn	Lys	Tyr
850			855								860				
Lys	Val	Leu	Val	Ser	Val	Asn	Ala	Ile	Arg	Arg	Thr	Tyr	Glu	Glu	Tyr
865			870								875				
His	Ala	Phe	Ser	Lys	Phe	Val	Pro	Met	Phe	Leu	Phe	Asn	Leu	Ile	Lys
			885								890				
Arg	Glu	Leu	Glu	Gly	Asp	Asn	Tyr	Thr	His	Asp	Val	His	Phe	Ser	Ser
900							905				910				
Thr	Cys	Leu	Trp	Tyr	Leu	Thr	Val	Met	Thr	Arg	Asn	Arg	Ile	Cys	Asp
915							920				925				
Val	Leu	Gln	Tyr	Ile	Asn	Asn	Asn	Asn	Asn	Asp	Asn	Glu	Glu	Thr	Asp
930			935								940				
Ile	Val	Glu	Glu	Glu	Glu	Glu	Gly	Glu	Gly	Glu	Glu	Asp	Lys	Met	Glu
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Glu	Ser	Met	Asp	Val	Glu	Gln	Gln	Lys	Gln	Val	Arg	Lys	Gly	Gly	Arg
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Lys	Lys	Gly	Gln	Lys	Phe	Asn	Ser	Ile	Gly	Asp	Gln	Val	Ile	Arg	Lys
			980				985				990				
Phe	Val	Lys	Ser	Leu	Cys	Glu	Asn	Ser	Met	Val	Val	Ser	Ile	Ala	Ile
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Asn	Ser	Leu	Ile	Ser	Gly	Ile	Ser	Trp	Met	Asn	Lys	Lys	Ile	Pro	Pro
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Arg	Phe	Val	Phe	Ser	Asp	Val	Lys	Ile	Asn	Arg	Lys	Ile	Asn	Gly	Thr
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Asp	Asp	Lys	Tyr	Glu	Thr	Val	Phe	Gly	Val	Ser	Thr	Arg	Val	Asp	Ser
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His	Ile	Val	Gly	Pro	Phe	Ser	Ile	Pro	Val	Asp	Phe	Ser	Ser	Ala	Gly
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Lys	Gly	Ile	Leu	Thr	Ile	Ser	Pro	Lys	Tyr	Asp	Ser	Leu	Asn	Asp	Glu
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Leu	Ser	Lys	His	Asp	Thr	Phe	Phe	Asn	Ile	Asn	Lys	Asn	Lys	Val	Leu
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1155							1160				1165				
Thr	Lys	Phe	Asn	Arg	Lys	Lys	Ile	Ser	Ser	Gly	Met	Ser	Asn	Asn	Asn
1170			1175								1180				
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1185			1190								1195				
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			1205								1210				
Leu	Ser	Ser	Thr	Lys	Lys	Lys	Ser	Ile	Trp	Asn	Glu	Asn	Met	Phe	Leu

Ser Pro Ser Asp Leu Asn Leu Cys Ile Tyr Thr Ser Ser Leu Asn Asp
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 1330 1335 1340
 Ala Leu Asp Asp Tyr Gly Ala Val Phe Val Asn Tyr Thr Phe Lys Ser
 1345 1350 1355 1360
 Ile Lys Ser Cys Ser Ser Lys Asp Glu Thr Ala Asp Asp Asn Ala Ala
 1365 1370 1375
 Ala Ala Asp Asp Asp Gly Ser Thr Thr Ser Thr Ser Ser Ser Thr Asp
 1380 1385 1390
 Thr Asp Ala Ala Ala Ile Gln Asp Phe Met His Val Met Ile Lys Lys
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 1425 1430

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 ggtgacgacg acgacgacga tgacgatgga ggaacttttcg atacagtagg gtctggtata 240
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 gatgatttct accgcaaaaa gcgtgccgca cctccacctg aggatgaaga agaggatgat 780
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 <212> PRT
 <213> SHRIMP

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 35 40 45
 Cys Gln Gly Arg Leu Cys Arg Arg Ser Thr Arg Gly Gly Asp Asp Asp
 50 55 60
 Asp Asp Asp Asp Gly Gly Thr Phe Asp Thr Val Gly Ser Gly Ile
 65 70 75 80
 Leu Gly Arg Lys Lys Arg Ala Ala Pro Pro Pro Glu Asp Glu Glu Glu
 85 90 95
 Asp Asp Phe Tyr Arg Lys Lys Arg Ala Ala Pro Pro Pro Glu Asp Glu
 100 105 110

Glu Glu Asp Asp Phe Tyr Arg Lys Lys Arg Ala Ala Pro Pro Pro Glu
 115 120 125
 Asp Glu Glu Glu Asp Glu Phe Tyr Arg Lys Lys Arg Ala Ala Pro Pro
 130 135 140
 Pro Glu Asp Glu Glu Glu Asp Glu Phe Tyr Arg Lys Lys Arg Ala Ala
 145 150 155 160
 Pro Pro Pro Glu Asp Glu Glu Glu Asp Glu Phe Tyr Arg Lys Lys Arg
 165 170 175
 Ala Ala Pro Pro Pro Glu Asp Glu Glu Glu Asp Glu Phe Tyr Arg Lys
 180 185 190
 Lys Arg Ala Ala Pro Pro Pro Glu Asp Glu Glu Glu Asp Glu Phe Tyr
 195 200 205
 Arg Lys Lys Arg Ala Ala Pro Pro Glu Asp Glu Glu Glu Asp Glu
 210 215 220
 Phe Tyr Arg Lys Lys Arg Ala Ala Pro Pro Pro Glu Asp Glu Glu Glu
 225 230 235 240
 Asp Asp Phe Tyr Arg Lys Lys Arg Ala Ala Pro Pro Pro Glu Asp Glu
 245 250 255
 Glu Glu Asp Asp Phe Tyr Arg Lys Lys Arg Ala Ala Pro Pro Pro Glu
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 Pro Glu Asp Glu Glu Glu Asp Asp Phe Tyr Arg Lys Lys Arg
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 aatagtgaac aaacagctaa aaaggaaggt ctagcaacta gagtggaaca gcaagccaca 180
 gagatacaac aattcaagga cgaaataaac aacaaatata atgctctaac aaatactttg 240
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 tgtgacgact tgtgcaatca attacaaaaa gaagaggaag aagaggaaga tttgaaacag 540
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 ttgacttttc taacagtgtg cactaatgtt atagcagaat ttataaacgc tagcaatatt 960
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 <211> 368
 <212> PRT
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Leu	Ala	Thr	Arg	Val	Ala	Lys	Gln	Ala	Thr	Glu	Ile	Gln	Gln	Phe	Lys
	50					55					60				
Asp	Glu	Ile	Asn	Asn	Lys	Tyr	Asn	Ala	Leu	Thr	Asn	Thr	Leu	Asp	Asp
65					70					75					80
Ile	Ile	Tyr	Ile	Phe	Asp	His	Gly	Gly	Ser	Phe	Lys	Arg	Ala	Lys	His
				85					90					95	
Lys	Ala	Ile	Ile	Glu	Ala	Arg	Glu	Tyr	Ser	Lys	Pro	Leu	Arg	Glu	Leu
			100					105					110		
Glu	Cys	Met	Phe	Thr	Arg	Ile	Ala	Asp	Met	Leu	Thr	Leu	Thr	Phe	Met
		115					120					125			
Thr	Val	Tyr	Thr	Asn	Ile	Ile	Thr	Glu	Phe	Arg	His	Ser	Ser	Glu	Gln
	130				135					140					
Ala	Thr	Asn	Ser	Ile	Asn	Val	Thr	Leu	Gly	Arg	Leu	Phe	Leu	Cys	Asp
145				150						155					160
Asp	Leu	Cys	Asn	Gln	Leu	Pro	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Leu
			165					170						175	
Lys	Gln	Lys	Phe	Ile	Thr	Phe	His	Ala	Asn	Leu	Tyr	Met	Leu	Asp	Thr
			180					185					190		
Arg	Leu	Lys	Lys	Asp	Leu	Ile	Ile	Phe	Lys	Asp	Val	Ile	Gln	Gln	Leu
		195					200					205			
His	Val	Ile	Leu	Gln	Lys	Asp	Thr	Tyr	Ala	Val	Lys	Glu	Gly	Val	Ala
	210					215					220				
Ile	Arg	Cys	Ala	Lys	Gln	Met	Asn	Glu	Ile	Ser	Gln	Tyr	Arg	Asp	Asn
225				230						235					240
Leu	Lys	Asp	Asn	Tyr	Asn	Thr	Phe	Ser	Asn	Ile	Leu	Asn	Glu	Ile	Val
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Tyr	Ile	Phe	Asp	His	Gly	Gly	His	Phe	Glu	Glu	Val	Lys	His	Lys	Ala
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Ile	Thr	Leu	Thr	Arg	Asn	Tyr	Leu	Lys	Thr	Leu	Met	Gly	Leu	Lys	Cys
	275					280					285				
Met	Phe	Lys	Arg	Ile	Ser	Glu	Met	Leu	Ser	Leu	Thr	Phe	Leu	Thr	Val
	290					295					300				
Tyr	Thr	Asn	Val	Ile	Ala	Glu	Phe	Ile	Asn	Asn	Ile	Ser	Asp	Arg	Glu
305				310						315					320
Ile	Asn	Asn	Tyr	Leu	Val	Gln	Leu	Val	Thr	Cys	Asn	Glu	Leu	Cys	Asn
			325						330					335	
Gln	Leu	Pro	Lys	Pro	Lys	Gln	Tyr	Arg	Pro	Leu	Ser	Leu	Ile	Asp	Asn
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cgagaagagt	tattggggaa	tctccctgaa	ggtgcagaaa	ttttcaggcc	tagagaagtt	360
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<210> 247

<211> 514

<212> PRT

<213> SHRIMP

<400> 247

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Asn Ser Leu Pro Asp Asp Gln Val Ile Ser Gln Phe Arg Tyr Phe Asp
35     40     45
His Arg His Cys Tyr Thr Phe Met Glu Ile Leu Met Ala Asn Ile Lys
50     55     60
Ile Gln Asp Arg Lys Gln Asn Thr Thr Ala Ile Cys Glu Leu Thr Thr
65     70     75     80
Gly Arg Glu Gly Leu Leu Cys Arg Arg Thr Ile Pro Val Phe Leu Gly
85     90     95
Ser Glu Glu Lys Arg Glu Glu Leu Leu Gly Asn Leu Pro Glu Gly Ala
100    105    110
Glu Ile Phe Arg Pro Arg Glu Val Met Gln Val Ile Gly Thr Leu Leu
115    120    125
Asp Lys Lys Leu Glu Ile Asp Asp Gly Ile Ala Ser Val Lys Ala Ala
130    135    140
Leu Cys Ala Gly Ser Ser Leu Tyr Leu Ile Met Ser His Ile Val
145    150    155    160
Lys Met Thr Phe Ser Ala Ile Thr Asn Met Lys Asp Ile Asn Glu Glu
165    170    175
Tyr Phe Val Asp Phe Ile Phe Arg His Lys Gln Phe Leu Asn Pro Glu
180    185    190
Phe Phe Lys His Leu Ile Ser Leu Leu Lys Asn Ser Arg Lys Glu His
195    200    205
Val Ala His Leu Val Arg Arg Leu Glu His Phe Leu Met Leu Trp Thr
210    215    220
Leu Ser Lys Met Arg Phe Thr Glu Met Glu Glu Asn Tyr Phe Pro Ile
225    230    235    240
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Pro Lys Tyr Lys Leu Arg Ile Phe Arg Glu Arg Lys Cys Cys Asp Arg
260    265    270
Cys Cys Arg Leu Tyr His Gln Gln Pro Pro Pro Glu Val Tyr Asn Trp
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Asp Gly Lys Ile Thr Gln Gln Ser Asn Lys Gly Tyr Ile Asn Ala Gly
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 Ile Pro Thr Cys Leu Phe Val Thr Cys Asn Lys Cys Asn Arg Ile Phe
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 Arg Leu Thr Ile Leu Gly Pro Thr Arg Asn Ile Leu Cys Pro Pro Cys
 370 375 380
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 385 390 395 400
 Pro Ser Phe Val Gln Lys Gly Thr Lys Arg Leu Arg Val Asp Thr Gly
 405 410 415
 Ser Asn Lys Asn Thr Leu Glu Lys Phe Cys Ser Trp Glu Arg Phe Asn
 420 425 430
 Thr Glu Val Leu Leu Pro Trp Leu Gly Tyr Thr Ile Glu Ser Lys Trp
 435 440 445
 Gln Asn Trp Glu Ser Phe Leu Gly Tyr Ser Ser Thr Arg Tyr Lys Glu
 450 455 460
 Leu Trp Ala Phe Val Asn Lys Gln Glu Ile Ser Ser Met Lys Asp Ser
 465 470 475 480
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 Gly Leu

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 <212> DNA
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<210> 249
 <211> 409
 <212> PRT

<213> SHRIMP

<400> 249

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Gln Val Ala Glu Ile Lys Ser Glu Tyr Lys Thr Glu Glu Glu Lys
 20      25      30
Arg Ile Ala Gln Glu Val Phe Asp Lys Phe Thr Lys Lys Leu Ile Met
 35      40      45
Gln Val Asp Thr Ser Lys His Leu Leu Thr Arg Glu Asn Pro Asn Arg
 50      55      60
Phe Val Ser Arg Pro Ile Val His Glu Asp Leu Trp Glu Met Tyr Lys
 65      70      75      80
Lys Glu Val Ala Cys Phe Trp Thr Leu Glu Glu Ile Asp Phe Glu Arg
 85      90      95
Asp Pro Lys Asp Trp Glu Lys Leu Thr Gln Asp Glu Lys Asp Phe Ile
 100     105     110
Leu Gln Ile Leu Ala Phe Phe Ala Ser Ser Asp Gly Ile Val Ile Glu
 115     120     125
Asn Leu Thr Thr Arg Leu Arg Gln Val Ala Gln Ile Pro Glu Ala Arg
 130     135     140
Ser Phe Phe Asp Phe Gln Val Gly Met Glu Ser Ile His Gly Asn Val
 145     150     155     160
Tyr Gly Glu Leu Ile Asp Arg Leu Val Pro Asp Glu Lys Asp Lys Ala
 165     170     175
Ile Leu Phe Asn Ala Ala Gln His Phe Pro Ala Ile Lys Lys Lys Glu
 180     185     190
Gln Trp Ala Ile Asn Trp Met Gln Ser Asn Asn Asp Leu Ala Glu Leu
 195     200     205
Ile Val Ala Phe Ala Ala Val Glu Gly Ile Phe Phe Ser Gly Ala Phe
 210     215     220
Ala Ser Ile Phe Trp Ile Lys Asn Arg Gly Ile Leu Pro Gly Leu Thr
 225     230     235     240
Ser Ser Asn Glu Phe Ile Ser Arg Asp Glu Gly Leu His Arg Asp Phe
 245     250     255
Ala Cys Met Leu Leu Lys Lys Gly Phe Val Asp Thr Pro Ser Arg Glu
 260     265     270
Arg Ile Ile Val Thr Glu Ala Val Arg Ile Glu Gln Glu Phe Leu Thr
 275     280     285
Val Ser Leu Pro Val Lys Leu Val Gly Met Asn Cys Lys Leu Met Ser
 290     295     300
Gln Tyr Ile Glu Phe Val Ala Asp Lys Leu Leu Val Glu Met Gly Leu
 305     310     315     320
Glu Lys His Tyr Asn Val Thr Asn Pro Phe Pro Phe Met Asp Asn Ile
 325     330     335
Ser Leu Glu Asn Lys Thr Asn Phe Phe Glu Lys Arg Val Ala Glu Tyr
 340     345     350
Gln Arg Ala Gln Val Met Ala Ser Ile Asn Lys Ile Lys Lys Asp Gln
 355     360     365
Gln Thr Gln Glu Thr Gly Ser Pro Leu Pro Ile Leu Thr Ala Pro Pro
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<210> 250

<211> 915

<212> DNA

<213> SHRIMP

<400> 250

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<210> 251

<211> 298

<212> PRT

<213> SHRIMP

<400> 251

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 20          25          30
Pro Leu Val Phe Asp Ser Val Leu Glu Glu Val Val Tyr Pro Thr Asp
 35          40          45
Val Cys Gly Pro Lys Gly Ala Gly Glu Leu Phe Thr Gly Val Asp Leu
 50          55          60
Leu Thr Leu Cys Ile Gly Gly Lys Asn Asn Gly Gly Glu Trp Ser Gly
 65          70          75          80
Lys Gly Pro Cys Pro Arg Ile Asn Asn Ala Val Val Glu Arg Asp Tyr
 85          90          95
Ser Leu Asp Glu Glu Asp Cys Lys Gly Phe Arg Lys Gly Phe Arg Ile
100          105          110
Pro Gly Thr Asp His Phe His Thr Val Phe Ser Leu Cys Trp Val Asp
115          120          125
Arg Asp Met His Ala Lys Trp Val Arg Asn Lys Ile Asn Pro Gly Ile
130          135          140
Val Thr Asp Asp Glu Asp Leu Val Asp Ser Gly Ile Arg Thr Lys Phe
145          150          155          160
Lys Tyr Ser Ser Lys Ile Phe Gly Lys Gly Phe Asn Pro Arg Pro Lys
165          170          175
Leu Asp Tyr Gln Glu Arg Ile Lys Ile Leu Lys Ser His Phe Asn Lys
180          185          190
Arg Thr Gly Asn Phe Phe Arg His Leu Ala Pro Ala Gly Asp Phe Phe
195          200          205
Leu Ala Ser Trp Ala Thr Phe Ala Leu Glu Asn Ala Val Pro Gln Ile
210          215          220
Gln Asn His Asn Asn Gly Glu Trp Lys Asp Ile Glu Asn Arg Ala Arg
225          230          235          240
Thr Thr Pro Gly Ala Ala Trp Ala Glu Thr Gly Pro Ile Phe Tyr Gln
245          250          255
His Lys Lys Lys Glu Tyr Leu Asp Lys Lys Lys Lys Tyr Ile Pro Ile
260          265          270
Pro His Ala Leu Tyr Lys Ile Val Tyr Asp Lys Asn Asn Lys Glu Leu
275          280          285

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Phe Arg Val Gln Ser Asp Met Ser Trp Lys
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<211> 789
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<212> PRT
<213> SHRIMP

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His Val Met Lys Ser Ile Ser Asp Tyr Ile Ile Ser Arg Arg Phe Met
35 40 45
Asn Tyr Thr Asn Leu Leu Lys Gln Val Glu Tyr Val Phe Asp Glu Glu
50 55 60
Thr Gly Ala Val Ile Ala Asn Ile Cys Leu Leu Lys Ile Arg Cys Ala
65 70 75 80
Gln Lys Gly Gly Ile Tyr Asp Ala Pro Glu Asp Val Ala Phe Phe Asn
85 90 95
Ser Lys Met Gly Glu Val Thr Arg Leu Phe Thr Ile Ile Gly Gly Arg
100 105 110
Pro Asn Met Thr Val Arg Val Asn Phe Lys His Gly Gln Thr Asn Asn
115 120 125
Pro Ala Tyr Gly Tyr Leu Thr Asp Asp Asn Asp Thr Thr Thr Val Thr
130 135 140
Pro Pro Val Thr Pro Pro Pro Ser Pro Ala Ala Arg Arg Ser Pro Phe
145 150 155 160
Phe Thr Arg Thr Leu Ile Ser Glu Ser Ser Ser Val Asp His Tyr Val
165 170 175
Leu Met His Asp Asn Pro Lys Arg Ser Ser Phe Lys Val Tyr Asp Ile
180 185 190
His Ala Glu Thr Phe Pro His Lys Ala Pro Ser Val Pro Thr Phe Pro
195 200 205
Pro Lys Thr Ser Phe Glu Ile Ser Asp Val Thr Leu Asp Cys Ser Met
210 215 220
Glu Ile Phe Ser Arg Asp Arg Asp Val Leu Asp Asn Val His Asp Tyr
225 230 235 240

Ile Ala Asn Asp Pro Val Pro Phe Leu Val Asp Val Val His Arg Gly
 245 250 255
 Ser Ser Leu Arg
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 <212> DNA
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 cctattgaaa caatatacga aatactctct tcttctgctg acgacaagaa gtttgtacag 360
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 <212> PRT
 <213> SHRIMP

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		20						25					30		
Pro	Phe	Pro	Val	Asp	Lys	Tyr	Arg	Ala	Val	Asp	Lys	Lys	Val	Val	Asn
		35					40					45			
Leu	Ile	His	Lys	Ile	Leu	Asp	Gln	Glu	Lys	Asp	His	Leu	Ser	Ser	Thr
	50					55					60				
Glu	Leu	Gln	Met	Ile	Thr	Glu	Cys	Asn	Gly	Ala	Arg	Glu	Asp	Leu	Leu
65					70					75					80
Lys	His	Leu	Leu	Asp	Glu	Gly	Glu	Phe	Asn	Pro	Thr	Ile	Ile	Glu	Val
				85					90					95	
Val	Ser	Ser	Met	Pro	Ile	Glu	Thr	Ile	Tyr	Glu	Ile	Leu	Ser	Ser	Ser
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		115					120					125			
Ile	Leu	Phe	Phe	Ala	Asp	Lys	Gly	Thr	Met	Trp	Val	Ser	Asn	Ala	Cys
	130					135					140				
Val	Gln	Asn	Val	Leu	Gly	Asn	Asp	Tyr	Lys	Val	Glu	Phe	Glu	Asn	Ile
145					150					155					160
Arg	Lys	Lys	Tyr	Leu	Ile	Asp	Leu	Leu	Asn	Gly	Val	Ser	Asn	His	Trp
				165					170					175	
Ser	Glu	His	Gly	Pro	Leu	Ser	His	Met	Leu	His	Ser	Ser	Ile	Pro	Ile
			180					185					190		
Val	Gln	Asp	Met	Leu	Leu	Asn	Arg	Leu	Val	Arg	Tyr	Phe	Ser	Thr	Tyr
		195					200					205			
Asp	Gly	Asp	Ala	Gln	Phe	Asp	Ile	Ser	Phe	Ile	Ile	Asn	Ser	Val	Leu
	210					215					220				
Trp	Gly	Ile	Asp	Lys	Ser	Val	Leu	Asn	Glu	Leu	Thr	Gln	Leu	Ile	Ser
225					230					235					240
Arg	Gly	Val	Phe	Ile	Val	Ser	Tyr	Val	Pro	Met	Arg	Val	Arg	Thr	Pro
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Ser	Lys	Asp	Ser	Asn	Arg	Pro	Gln	Asn	Thr	Pro	Ser	Gln	Asn	Met	Ser
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Ala	Leu	Gly	Met	Lys	Leu	Asn	Thr	Phe	Ser	Ser	Arg	Ile	Ser	Val	Tyr
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Arg	Asn	Asn	Thr	Phe	Lys	Lys	Leu	Thr	Glu	Leu	Val	His	Asn	Phe	Asp
	290					295					300				
Tyr	Gly	Ser	Lys	Asp	Ala	Ser	Ser	Ser	Ser	Pro	Pro	Pro	Pro	Ser	Leu
305					310					315					320
Ser	Asp	Ser	Val	Asn	Thr	Phe	Val	Arg	Leu	Tyr	Thr	Asn	Tyr	Asp	Ile
				325					330					335	
Phe	Leu	Lys	Val	Ile	Ser	Asp	Trp	Lys	Met	Pro	Tyr	Gly	Phe	Phe	Lys
			340					345					350		
Lys	Thr	Phe	Asp	Val	Lys	Lys	Gly	Leu	Met	Thr	Leu	Ser	Val	Ser	Glu
		355					360					365			
Tyr	Thr	Leu	Lys	Lys	Glu	Leu	Val	Thr	Phe	Leu	Arg	Ala	Leu	Lys	Glu
	370					375					380				
Arg	Glu	Ile	Leu	Ile	Tyr	Lys	Met	Glu	Lys	Arg	Asp	Ile	Ile	Cys	Ile
385					390					395					400
Leu	Lys	Lys	Ser	Leu	Phe	Gly	Phe	Asn	Phe	Arg	Cys	Leu	Lys	Gln	Leu
				405					410					415	
Leu	Pro	Leu	Phe	Lys	His	Phe	Leu	Lys	Ile	Glu	Glu	Val	Lys	His	Ile
			420					425					430		
Ala	Arg	Phe	Val	Phe	Arg	Asp	Tyr	Ser	Leu	Met	Cys	Lys	Thr	Gln	Lys
		435					440					445			
Asp	Leu	Gln	Ser	Phe	Pro	Ala	Ile	Gln	Ser	Ala	Ser	Leu	Phe	Met	Glu
	450					455					460				
Glu	Phe	Pro	Trp	Leu	Ala	Lys	Thr	Trp	Ile	Asp	Asp	Asp	Asp	Asp	Glu
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Gly Gly Lys Gly His Thr Leu Leu Thr Phe Ala Ile Val His Arg Tyr
 485 490 495
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 Asn Thr Thr Cys Arg Asp Lys His Phe Thr Pro Leu Met His Leu Ala
 515 520 525
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 530 535 540
 Asn Gly Ala Lys Pro Glu Phe Ile Asn Lys Phe Asn Glu Asn Val Leu
 545 550 555 560
 His Ile Ala Ile Glu Asn Val Asn Tyr Gly Val Ile Thr Glu Leu Arg
 565 570 575
 Gly Thr Leu Ser Ser Glu Gln Ile Glu Lys Met Val Asn Val Arg Arg
 580 585 590
 Met Met Asp Asn Thr Thr Pro Leu Met Ile Ala Arg Glu Asn Ile Val
 595 600 605
 Leu Ala Gln Leu Phe Asp Gly Lys Pro Lys Ile Lys Val Arg Phe Gly
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 Lys Glu Ser Val Ala Tyr Leu Glu Thr Arg Asn Ile Ser Tyr Asp Ile
 645 650 655
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 660 665 670
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 675 680 685
 Ala Asp Glu Lys Thr Met Asn Thr Trp Asn Phe Phe Thr Lys Asn Ser
 690 695 700
 Thr Lys Trp Ala Ser Ser Ile Phe Gln Lys Asn Arg Gln Lys Phe Val
 705 710 715 720
 Lys Ile Val Asp Gly Met Asn Arg Thr Tyr Glu Asp Ser Glu Cys Ala
 725 730 735
 Ile Cys Leu Asp Ser Leu Asp Gly Asp Leu Pro Ser Gly Arg Thr Thr
 740 745 750
 Cys Gly His Cys Phe His Asn Val Cys Trp Leu Ser Leu Ile Arg Met
 755 760 765
 Ser Gly Pro Asn Asn Gly Ser Arg Arg Gly Gly Ile Lys Cys Pro Ser
 770 775 780
 Cys Arg Gln Val Thr Cys Leu Gly Lys Arg Leu Gly Val Ala Asp Tyr
 785 790 795 800
 Asp Ile Glu Thr Glu Glu Glu Arg Asp Thr Lys Asn Val Val Pro Ser
 805 810 815
 Val Glu Glu Gly Arg Arg Glu Trp Arg Lys Ile Gly Val Asp Arg Tyr
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 835 840 845

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 aaggacctgg acatctctga acccatgctc aaatctacca cttacgatct ggccaatgtt 300
 acccctcaag tcacaaaact ggtaacattt tctgggtccaa cctatgctag tccgcctaca 360
 cccaggccag ttgccaatac acctcaacaa caaccaacaa gtacaaataa agaggaagaa 420

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<210> 257
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 <212> PRT
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<400> 257

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		20						25				30			
Met	Leu	Val	Lys	Cys	Ile	Asp	Arg	Thr	Thr	Thr	Cys	Ile	Ser	Cys	Ser
		35					40					45			
Pro	Trp	Glu	Lys	Asn	Lys	Asn	Lys	Lys	Asn	Arg	Asn	Gly	Ser	Asn	Thr
	50					55					60				
Glu	Ser	Ser	Phe	Ile	Ser	His	Val	Arg	Phe	Asn	Thr	Pro	Asp	Lys	Asp
65					70					75				80	
Leu	Asp	Ile	Ser	Glu	Pro	Met	Leu	Lys	Ser	Thr	Thr	Tyr	Asp	Leu	Ala
				85					90					95	
Asn	Val	Thr	Pro	Gln	Val	Thr	Lys	Leu	Val	Thr	Phe	Ser	Gly	Pro	Thr
			100					105					110		
Tyr	Asp	Pro	Thr	Pro	Arg	Pro	Val	Ala	Asn	Thr	Pro	Gln	Gln	Gln	Pro
		115					120					125			
Thr	Ser	Thr	Asn	Lys	Glu	Glu	Glu	Ser	Val	Tyr	Met	Pro	Met	Ser	Ser
		130				135					140				
Cys	Ser	Ser	Ser	Phe	Ser	Ser	Asp	Asn	Ser	Leu	Pro	Leu	Pro	Thr	Pro
145					150					155				160	
Pro	Pro	Ser	Pro	Pro	Arg	Ser	Asn	Gly	Gly	Asp	Tyr	Val	Ser	Tyr	Val
			165					170						175	
Asn	Gly	Arg	His	Leu	Lys	Leu	Pro	Ser	Asn	Pro	Pro	Ser	Pro	Ile	Phe
			180					185					190		
Asn	Ile	Lys	Asn	Glu	Glu	Gly	Glu	Asp	Asp	Asn	Val	Glu	Glu	His	Val
		195					200					205			
Tyr	Glu	Tyr	Val	Pro	Glu	Val	Pro	Gln	Gln	Ser	Pro	Ser	Ile	Gln	Lys
	210					215					220				
Cys	Ile	Gln	Glu	Leu	Lys	Glu	Met	Lys	His	Lys	Lys	Asn	Thr	Leu	Thr
225					230					235				240	
Arg	Ser	Ser	Ser	Asn	Asn	Asn	Asn	Asn	Ala	Pro	Arg	Ile	Thr	Gln	Val
			245						250					255	
Thr	Phe	Lys	Lys	Phe	Pro	Pro	Asn	Asn	Asn	Asn	Met	Trp	Glu	Asn	His
			260					265					270		
Val	Tyr	Gly	Asn	Thr	Thr	Ile	Val	Ser	Ser	Thr	Pro	Ser	Pro	Thr	Phe
		275					280					285			
Ile	Pro	Ser	Pro	Lys	Ser	Ile	Ile	Arg	Lys	Leu	Ser	Phe	Lys	Arg	Lys
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Gln															
305															

<210> 258
 <211> 549
 <212> DNA

<213> SHRIMP

<400> 258

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tgtcattctg taaacgtgcc agatgttggtg cctaatacaa tatttgcagt tttcttaoct 240
gaagaggacc gtgccaataa ccccgggcta tacgattcta ttgaaggagt atgtataaca 300
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gtgtccttgc ataaggactt atttggtgaa gatattcttg atggaataga aactgcatca 420
agggagaagt ctcggtctat ccacctatat ctggaggctg ggcagagtat cagaaccca 480
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<210> 259

<211> 180

<212> PRT

<213> SHRIMP

<400> 259

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  20           25           30
Met Arg Lys Asp Phe Pro Ser Thr Phe Leu Gln Cys Arg Met Ile Asp
  35           40           45
Phe His Phe Ser Gly Asp Ile Ile Asp Lys His Tyr Cys His Ser Val
  50           55           60
Asn Val Pro Asp Val Val Pro Asn Thr Ile Phe Ala Val Phe Leu Pro
  65           70           75           80
Glu Glu Asp Arg Ala Asn Asn Pro Gly Asp Ser Ile Glu Gly Val Cys
  85           90           95
Ile Thr Val Glu Gln Gly Glu Leu Cys Ile Ile Asn Lys Ser Ser Val
  100          105          110
His Glu Phe Asn Ile Leu Val Ser Leu His Lys Asp Leu Phe Gly Glu
  115          120          125
Asp Ile Leu Asp Gly Ile Glu Thr Ala Ser Arg Glu Glu Ser Arg Ser
  130          135          140
Ile His Leu Tyr Leu Glu Ala Gly Gln Ser Ile Arg Thr Pro Ile Pro
  145          150          155          160
Arg Pro Glu Gly Thr Asn Thr Val Asn Tyr Thr Ile Val Phe Ser Asn
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Gln Val Thr Val
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<210> 260

<211> 3543

<212> DNA

<213> SHRIMP

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gctgaccctg cgttattggc gctagcggca caacaagaag atgcgacaat tatacctgaa 480
aaccagtgga aaagtatagt gaacaccccc tcgccagtag ggccaaatag gcaagttctt 540

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cccatgttga actttttact tgaaaatgtg aacgccatgg gcggatcagc aggtgaagaa 600
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gaaaaagaac ctatagaaca agaaaaaaat gaacccgaga aggatgaaga tgcaatagaa 780
aatgaaagcg tgcactctca tagagttgaa tccagcccta tgagtgaagg aggtaatgat 840
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cttttgaata acaaatctag cgtcaattct ctagcaaagc aagtgaaaag aatgaagcac 3480
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<210> 261
<211> 1174
<212> PRT
<213> SHRIMP

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Glu	Asp	Glu	Glu	Asp	Glu	Glu	Glu	Met	Asn	Glu	Asp	Glu	Glu	Glu	Glu	Glu
		35					40					45				
Glu	Glu	Glu	Asp	Tyr	Glu	Asp	Glu	Asp	Glu	Asp	Thr	Gly	Val	Arg	Asn	
	50					55					60					
Gly	Arg	Asn	Lys	Asp	Pro	Pro	Ser	Ser	Lys	Lys	Gln	Ser	Lys	Phe	Val	80
65					70					75						
Arg	Asp	Val	Thr	Asn	Asp	Met	Tyr	Asp	Asp	Asp	Asp	Glu	Glu	Glu	Glu	Glu
				85					90					95		
Glu	Glu	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Gly	Glu	Glu	Gly	Gly	Glu	Tyr	
			100					105					110			
Asp	Gly	Asn	Leu	Glu	Asp	Glu	Glu	Glu	Glu	Gly	Asp	Glu	Tyr	Glu	Asp	
		115					120					125				
Asp	Asn	Glu	Gly	Glu	Gly	Glu	Glu	Asp	Glu	Ala	Asp	Pro	Ala	Leu	Leu	
	130					135					140					
Ala	Ala	Gln	Gln	Glu	Asp	Ala	Thr	Ile	Ile	Pro	Glu	Asn	Gln	Trp	Lys	
145					150					155						
Ser	Ile	Val	Asn	Thr	Pro	Ser	Pro	Val	Gly	Pro	Asn	Arg	Gln	Val	Leu	
				165					170					175		
Pro	Met	Leu	Asn	Phe	Leu	Leu	Glu	Asn	Val	Asn	Ala	Met	Gly	Gly	Ser	
			180					185					190			
Ala	Gly	Glu	Glu	Gln	Lys	Asn	Lys	Glu	Asp	Asp	Asn	Gln	Gln	Ile	Glu	
		195					200					205				
Pro	Val	Glu	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Gln	Glu	Glu	Glu
	210					215					220					
Glu	Glu	Glu	Glu	Glu	Glu	Gln	Glu	Glu	Glu	Glu	Glu	Glu	Lys	Glu	Pro	
225					230					235					240	
Ile	Glu	Gln	Glu	Lys	Asn	Glu	Pro	Glu	Lys	Asp	Glu	Asp	Ala	Ile	Glu	
				245					250				255			
Asn	Glu	Ser	Val	His	Ser	His	Arg	Val	Glu	Ser	Ser	Pro	Met	Ser	Glu	
			260					265					270			
Gly	Gly	Asn	Asp	Asp	Gly	Met	Asp	Tyr	Phe	Phe	Ser	Ser	Ile	Ala	Gly	
		275					280					285				
Gly	Gly	Asn	Asp	Asn	Glu	Glu	Asp	Glu	Glu	Glu	Asp	Glu	Glu	Glu	Gly	
	290					295					300					
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Pro	Ala	Gln	Lys	Ser	Glu	Glu	His	Val	
305						310				315					320	
Glu	Thr	Lys	Glu	Ser	Val	Gln	Ser	His	Thr	Glu	Tyr	Ile	Glu	Glu	Glu	Glu
				325					330					335		
Glu	Glu	Tyr	Glu	Glu	Tyr	Glu	Asp	Glu	Ser	Arg	His	Thr	Leu	Glu	Asp	
			340					345					350			
Glu	Glu	Ile	Ser	Thr	Met	His	Gln	Phe	Asn	Asn	Ala	Pro	Arg	Val	Arg	
		355					360					365				

Asn	Thr	Leu	Gly	Gly	Lys	Glu	Ala	Glu	Glu	Arg	Leu	His	Lys	Thr	Met
		515					520					525			
Glu	Ser	Ile	Ile	Leu	Lys	Thr	Arg	Val	Lys	Thr	Leu	Leu	Glu	Thr	Thr
		530					535				540				
Lys	Asn	Leu	Gln	Cys	Ser	Glu	Leu	Val	Lys	Val	Val	Phe	Gln	Asp	Pro
545					550					555					560
Glu	Asn	Pro	Val	Lys	Pro	Ser	Glu	Lys	Val	Met	Glu	Arg	Leu	Lys	Asn
				565					570					575	
Ile	Ile	Ala	Ala	Glu	Leu	Thr	Met	Lys	Ala	Phe	Leu	Asp	Ser	Ala	Ala
		580						585					590		
Val	Thr	Asp	Ile	Lys	Ser	Ala	Glu	Leu	Phe	Arg	Lys	Thr	Asn	Glu	Lys
		595					600					605			
Leu	Glu	Leu	Phe	Gln	Arg	Lys	Gln	Ile	Met	Ser	Asn	Pro	Leu	Phe	Ser
		610					615					620			
Ala	Ala	Tyr	Ala	Ser	Thr	Tyr	Ile	Met	Gly	Glu	Arg	Ala	Ser	Lys	Ile
625					630					635					640
Arg	Pro	Ser	Thr	Pro	Ala	Pro	Ser	Leu	Lys	Lys	Val	Glu	Ser	Ile	Ser
				645					650					655	
Glu	Leu	Asn	Glu	Asp	Glu	Thr	Ser	Met	Ser	Ser	Ser	Ala	Gly	Gly	Val
			660					665					670		
Cys	Ala	Glu	Gly	Asp	Glu	Ser	Ile	Ala	Gly	Gly	Gly	Gly	Gly	Gly	Gly
		675					680					685			
Gly	Gly	Gly	Gly	Glu	Val	Val	Glu	His	Ser	Ser	Phe	Tyr	Ser	Asn	Gln
		690				695					700				
Thr	Gln	Ala	Asn	Leu	His	Met	Glu	Leu	Ile	Asn	Ile	Leu	Lys	Glu	Asp
705					710					715					720
Asp	Asp	Asn	Gln	Pro	Cys	Gln	Thr	Tyr	Lys	Leu	Gly	Gln	Arg	Leu	Ala
			725						730					735	
Phe	Leu	Asn	Asn	Leu	Ile	Ser	Phe	Lys	Thr	Ser	Ser	Ala	Val	Ser	Trp
		740						745					750		
Ser	Arg	Leu	Val	Asn	Met	Leu	Ser	Asp	Ile	Val	Thr	Lys	Ala	Ser	Val
		755					760					765			
Phe	Gly	Asp	Thr	Asn	Lys	Ala	Gln	Glu	Asp	Phe	Glu	Lys	His	Gln	Thr
		770				775					780				
Glu	Thr	Asn	Asp	Val	Ser	Asp	Leu	Ser	Thr	Ser	Ser	Lys	Leu	Lys	Gln
785					790					795					800
Met	Ser	Lys	Glu	Ser	Ala	Asn	Ile	Met	Glu	Glu	Met	Gly	Leu	Gly	Ser
				805					810					815	
Ile	Gly	Ala	Glu	Ile	Cys	Phe	Gly	Ala	Ile	Ser	Thr	Ile	Ile	Glu	Lys
		820					825						830		
His	Ile	Asn	Lys	Leu	Cys	Met	Asp	Val	Gly	Arg	Leu	Thr	Ile	Phe	Leu
		835					840					845			
Asn	Ile	Pro	Ile	Val	Leu	Leu	Asn	Trp	Pro	Lys	Glu	Phe	Thr	Leu	Ser
		850				855					860				
Lys	Asp	Tyr	Lys	Val	Leu	Leu	Leu	Asp	Ser	Ile	Ser	Ser	Cys	Ser	Ser
865					870					875					880
Lys	Met	Ala	Val	Pro	Pro	Ile	Tyr	Val	Leu	Asn	Ser	Ile	Gln	Phe	Asp
				885					890					895	
Lys	Ala	Val	Asp	Glu	Glu	Asp	Glu	Asp	Gly	Asn	Gly	Ser	Glu	Ala	Glu
			900					905					910		
Lys	Arg	Ser	Glu	Asp	Gly	Asn	Met	Phe	Ser	Glu	Lys	Asp	Lys	Lys	Glu
		915					920					925			
Ala	Ile	Arg	Arg	Val	Tyr	Asp	Asn	Ile	Arg	Tyr	Gly	Asp	Ser	Asn	Asp
		930				935					940				
Arg	Thr	Ser	Leu	Asn	His	Phe	Phe	Gly	Asp	Ala	Tyr	Ser	Gly	Val	Ser
945					950					955					960
Asn	Asn	Asn	Ser	Lys	Asn	Ser	Met	Phe	Asp	Leu	Gln	Thr	Gln	Gly	Gly
				965					970					975	
Gly	Arg	Phe	Gly	Val	Ala	Tyr	Ser	Ala	Gly	Ser	Ser	Ile	Ile	Glu	His
			980					985					990		
Arg	Ser	Pro	Ile	Phe	Asp	Asn	Ala	Leu	Asn	Thr	Leu	Val	Asn	Phe	Met

995 1000 1005
 Asp Lys Arg Lys His Leu Leu Ser Ala Val Val Ile Lys Leu Leu Lys
 1010 1015 1020
 Lys Ala Lys Leu Ser Ile Glu Val Tyr Cys Ile Lys Tyr Lys Leu Asn
 1025 1030 1035 1040
 Gln Ala Ser Glu Lys Tyr Asn Lys Lys Gly Lys His Gly Lys Ser Thr
 1045 1050 1055
 Ser Val Val Pro Met Arg Asn Leu Met Tyr Arg Pro Ser Lys Asn Gln
 1060 1065 1070
 Asp Val Ser Pro Ser Thr Pro Ala Ala Ala Thr Ala Met Asp Val Pro
 1075 1080 1085
 Ser Ser Val Ser Ser His Val Gly Arg Lys Arg Thr Phe Ser Phe Ser
 1090 1095 1100
 Asn Asp Ile Asn Ser Asn Met Ser Ser Ala Ser Ser Val Tyr Ile Asp
 1105 1110 1115 1120
 Gln Glu Ser Ser Thr Pro Ser Arg Arg Arg Thr Phe Met Asp Leu Leu
 1125 1130 1135
 Asn Asn Lys Ser Ser Val Asn Ser Leu Ala Lys Gln Val Lys Arg Met
 1140 1145 1150
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 Glu Asp Asp Gln Tyr Glu
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 <212> DNA
 <213> SHRIMP

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 aacgaattgt tgaagaacac tgtaagacat ggagacagag tttacatgaa ggatgcagaa 180
 ctggatgtga gatctcgctt agaagacata aaaaaggatt gtgtttttaa ggcaattgaa 240
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 caaaatcttg tacattggta tcggcccccata atattcttgca cagatataga cgaaaaaatt 360
 caacaagaaa ctggtcaagt agggcggtgt agtgttgcta cgtacaattt gagaattggt 420
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 gtagtcatat tctttaatgt gattgttgaa gggaagagta aagatattga tattgtatgt 660
 aaatctagat ataaacacac ccatatacta aacggagaat ctgcaacata cgctgttaaa 720
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<210> 263
 <211> 261
 <212> PRT
 <213> SHRIMP

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 Asp Lys Ile Val Glu Arg Arg Gly Val Ser Asn Leu Ser Glu Leu Leu
 20 25 30
 Ile His Pro Ile Thr Lys His Ile Asn Glu Leu Leu Lys Asn Thr Val
 35 40 45
 Arg His Gly Asp Arg Val Tyr Met Lys Asp Ala Glu Leu Asp Val Arg
 50 55 60
 Ser Arg Leu Glu Asp Ile Lys Lys Asp Cys Val Leu Lys Ala Ile Glu

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65              70              75              80
Lys Gln Gly Ile Asp Val Arg Gln Ile Ile Thr Asp Tyr Leu Ala Lys
      85              90              95
Arg Lys Leu Thr Gln Asn Leu Val His Trp Tyr Arg Pro Pro Ile Ser
      100              105              110
Cys Thr Asp Ile Asp Glu Lys Ile Gln Gln Glu Thr Gly Gln Val Gly
      115              120              125
Arg Cys Ser Val Ala Thr Tyr Asn Leu Arg Ile Gly Gly Asp Asp Gly
      130              135              140
Glu Phe Thr Arg Tyr Asp Phe Ser Ile Pro Leu Gly Asp Phe Lys Ile
145              150              155              160
Thr Ala Lys Leu Phe Arg Ser Ile Asn Asp Glu Asp Val Asp Ala Val
      165              170              175
Ile Leu Val Ser Arg Ser Asp Val Val Asn Asp Val Leu Ser Phe Glu
      180              185              190
Ala Phe Asn Arg Thr Gly Glu Arg Val Val Ile Phe Phe Asn Val Ile
      195              200              205
Val Glu Gly Lys Ser Lys Asp Ile Asp Ile Val Cys Lys Ser Arg Tyr
210              215              220
Lys His Thr His Ile Leu Asn Gly Glu Ser Ala Thr Tyr Ala Val Lys
225              230              235              240
Arg Ile Lys Arg Gly Asp Thr Arg Asp Asp Ile Leu Phe Ala Ile Thr
      245              250              255
Ala Phe Lys Glu Glu
      260

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<210> 264
 <211> 852
 <212> DNA
 <213> SHRIMP

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gatcaagtaa ggcaagaaat caatagccat ttaactaatg taatgacttt tgaacatctt 240
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gatttaagtt tatcgttcaa aatagattct tcagccaaaa ctctcacgtt agaatttaac 600
cgcaaatcca cgttcgctgg tattgtaaac agacccaaaa gtgtagtgat attatcaaat 660
ctaagaaata gtgattcttc tgataacata ggtgattatc taaagagaaa tgatcctata 720
tatattagtc atgatacaaa tggcataatc aaccatccg aggattcggc ctctctcatt 780
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<210> 265
 <211> 283
 <212> PRT
 <213> SHRIMP

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      20              25              30
Thr Arg Lys Ser Asp Gln Leu Lys Tyr Arg Leu Gly Ala Ile Ala Tyr
      35              40              45

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Ser Val Ala Lys Asn Ala Ser Ile Lys Tyr Ile Glu Asp Gln Val Arg
 50 55 60
 Gln Glu Ile Asn Ser His Leu Thr Asn Val Met Thr Phe Glu His Leu
 65 70 75 80
 Tyr Glu Asp Ala Phe Asn Pro Val Ile Cys Glu Ala Ile Phe Glu Lys
 85 90 95
 Gly Ile Pro Val Val Met Glu Lys Val Tyr Asp Val Asn Arg Arg Ile
 100 105 110
 Met Glu Pro Arg Glu Asp Phe Ile Thr Glu Ile Leu Lys Glu Glu Arg
 115 120 125
 Trp Arg Arg Tyr Ile Pro Gly Phe Tyr His Thr Ser Phe Ser Phe Lys
 130 135 140
 Tyr Asn Thr Ile Ala Phe Thr Asp Ser Ser Thr Ser Phe Ser Val Pro
 145 150 155 160
 Ile Asn Asp Lys His Met Leu Ser Ile Thr Pro Pro Gly Ala Ala Gln
 165 170 175
 Gly Asp Leu Ile Asp Leu Ser Leu Ser Phe Lys Ile Asp Ser Ser Ala
 180 185 190
 Lys Thr Leu Thr Leu Glu Phe Asn Arg Lys Ser Thr Phe Ala Gly Ile
 195 200 205
 Val Asn Arg Pro Lys Ser Val Val Ile Leu Ser Asn Leu Arg Asn Ser
 210 215 220
 Asp Ser Ser Asp Asn Ile Gly Asp Tyr Leu Lys Arg Asn Asp Pro Ile
 225 230 235 240
 Tyr Ile Ser His Asp Thr Asn Gly Ile Ile Asn Pro Ser Glu Asp Ser
 245 250 255
 Ala Ser Leu Ile Thr Ile His Met Pro Glu Ile Glu Asn Ala Ser Asp
 260 265 270
 Asp Leu Tyr Ile Asp Phe Asn Leu Phe Val Phe
 275 280

<210> 266
 <211> 1302
 <212> DNA
 <213> SHRIMP

<400> 266
 atggcacttt caaacaatgg aggaatatac attgtttttg cggttattgt tttggtaata 60
 ggagcttcta ttgccctctt ctttgctatc tcgggcgtag ggaaggggaac tctacattca 120
 aatgccaaaa caaaaaagag taagaaatat aaattagact ctaaaatacac tgacgatgat 180
 gaaaaaactg acgacgataa taataataat ggaggaggag ggggaggaac agttgatgtt 240
 atcaatgaga cagcgcttca acgtcaaacg agagagcatt ttgcaagaac tcttgaaaaa 300
 gctgaggatg aattcttcac caaattagca gatcaggaat ttgacacata caaatcagaa 360
 aacgtatggt taataaagga taaaataaca gatggaaaag tttcaatccc tgaaggtgac 420
 ataaacgtcc ccgatgtcgg acaggcaatt gctgatgaaa acttgttcga tctcataggg 480
 acgaaccatg acgaagtcaa ggaaacgatg gatgaagttg ttgcacaaaa atctaccaat 540
 atcacttacg aacaactcgt aatagacttg accaatatatt tattgttttg tacagtaaca 600
 gttgatcctt ctgatgaaaa tggggatgaa agcctacaga gatcaacaga cccagacgca 660
 gaaatggtga tgttgacaac aacaccttct tcacaactag ctagacaaca acaacctcct 720
 caacctacac ctgattacct tgcccggtag tcaaaggaat tgggtgataaa taatatacga 780
 ggagggtttta tcagtgatcg tgatatgcgc acttggaag gacgaatgtc tgtacatgtc 840
 aacatgaaac agaggacatt taatgttatt agtgcagcaa cgaatctgga ttctctacaa 900
 gttggattag aacccgtgct aaaaaaaca ggtagagcag ctgtgggagg acgtattgaa 960
 aaagcccgga tagagttttc atttgtagta gaaggtaacc gtgtacgggt atacgctaca 1020
 aacaaaacag aggactgttt ttgtagttta tcgcccaact gttataatgt taaaaaggca 1080
 tcagactatt ggataagctc tgcaagcaca gctaaggaaa aaacgtactt gtttattgct 1140
 aataaaaaatg atgaaacaag tttcttctat aactttgagg aaggtgttga agaaattgac 1200
 ctggacattt ttatgacaat agattgtgca cctaactctt ctttcattaa aaatttacca 1260
 agacctatta cagataataa tataatggtt gcaactgtcat aa 1302

<210> 267
 <211> 431
 <212> PRT
 <213> SHRIMP

<400> 267

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			20					25					30		
Val	Gly	Lys	Gly	Thr	Leu	His	Ser	Asn	Ala	Lys	Thr	Lys	Lys	Ser	Lys
		35					40					45			
Lys	Tyr	Lys	Leu	Asp	Ser	Lys	Tyr	Thr	Asp	Asp	Asp	Glu	Lys	Thr	Asp
	50					55					60				
Asp	Asp	Asn	Asn	Asn	Asn	Gly	Gly	Gly	Gly	Gly	Gly	Thr	Val	Asp	Val
65					70					75				80	
Ile	Asn	Glu	Thr	Ala	Leu	Gln	Arg	Gln	Thr	Arg	Glu	His	Phe	Ala	Arg
				85					90					95	
Thr	Leu	Glu	Lys	Ala	Glu	Asp	Glu	Phe	Phe	Thr	Lys	Leu	Ala	Asp	Gln
			100					105					110		
Glu	Phe	Asp	Thr	Tyr	Lys	Ser	Glu	Asn	Val	Trp	Leu	Ile	Lys	Asp	Lys
		115					120					125			
Ile	Thr	Asp	Gly	Lys	Val	Ser	Ile	Pro	Glu	Gly	Asp	Ile	Asn	Val	Pro
	130					135					140				
Asp	Val	Gly	Gln	Ala	Ile	Ala	Asp	Glu	Asn	Leu	Phe	Asp	Leu	Ile	Gly
145					150					155				160	
Thr	Asn	His	Asp	Glu	Val	Lys	Glu	Thr	Met	Asp	Glu	Val	Val	Ala	Gln
				165					170					175	
Lys	Ser	Thr	Asn	Ile	Thr	Tyr	Glu	Gln	Leu	Val	Ile	Asp	Leu	Thr	Asn
			180					185					190		
Ile	Leu	Leu	Phe	Gly	Thr	Val	Thr	Val	Asp	Pro	Ser	Asp	Glu	Asn	Gly
		195					200					205			
Asp	Glu	Ser	Leu	Gln	Arg	Ser	Thr	Asp	Pro	Asp	Ala	Glu	Met	Val	Met
	210					215					220				
Leu	Thr	Thr	Thr	Pro	Ser	Ser	Gln	Leu	Ala	Arg	Gln	Gln	Gln	Pro	Pro
225					230					235				240	
Gln	Pro	Thr	Pro	Asp	Tyr	Leu	Ala	Arg	Tyr	Ser	Lys	Glu	Leu	Val	Ile
				245					250				255		
Asn	Asn	Ile	Arg	Gly	Gly	Phe	Ile	Ser	Asp	Arg	Asp	Met	Arg	Thr	Trp
			260					265					270		
Gln	Gly	Arg	Met	Ser	Val	His	Val	Asn	Met	Lys	Gln	Arg	Thr	Phe	Asn
		275					280					285			
Val	Ile	Ser	Ala	Ala	Thr	Asn	Leu	Asp	Ser	Leu	Gln	Val	Gly	Leu	Glu
	290					295					300				
Pro	Val	Leu	Gln	Lys	Gln	Gly	Arg	Ala	Ala	Val	Gly	Gly	Arg	Ile	Glu
305					310					315				320	
Lys	Ala	Arg	Ile	Glu	Phe	Ser	Phe	Val	Val	Glu	Gly	Asn	Arg	Val	Arg
				325					330					335	
Val	Tyr	Ala	Thr	Asn	Lys	Thr	Glu	Asp	Cys	Phe	Cys	Ser	Leu	Leu	Pro
			340				345						350		
Asn	Cys	Tyr	Asn	Val	Lys	Lys	Ala	Ser	Asp	Tyr	Trp	Ile	Ser	Ser	Ala
		355					360					365			
Ser	Thr	Ala	Lys	Glu	Lys	Thr	Tyr	Leu	Phe	Ile	Ala	Asn	Lys	Asn	Asp
	370					375					380				
Glu	Thr	Ser	Phe	Phe	Tyr	Asn	Phe	Glu	Glu	Gly	Val	Glu	Glu	Ile	Asp
385					390					395				400	
Leu	Asp	Ile	Phe	Met	Thr	Ile	Asp	Cys	Ala	Pro	Asn	Leu	Pro	Phe	Ile
				405					410					415	
Lys	Asn	Leu	Pro	Arg	Pro	Ile	Thr	Asp	Asn	Asn	Ile	Met	Val	Ser	
			420					425					430		

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359

<210> 268
 <211> 207
 <212> DNA
 <213> SHRIMP

<400> 268
 atgtctgata tgaccagaaa catcatcgtc ggcttggccg ttgtcgatcat cgcattgagc 60
 atggctcgctt tcatgctttc tgttactcct gcacttaccg gattcctcct aggtttgggt 120
 gtatcagcac taggagttac actcttttga tgtccacta tgaaatctcc agggggagga 180
 aatgctacaa tcaaccccgt ggcataa 207

<210> 269
 <211> 68
 <212> PRT
 <213> SHRIMP

<400> 269
 Met Ser Asp Met Thr Arg Asn Ile Ile Val Gly Leu Ala Val Val Val
 1 5 10 15
 Ile Ala Leu Ser Met Val Ala Phe Met Leu Ser Val Thr Pro Ala Leu
 20 25 30
 Thr Gly Phe Leu Leu Gly Leu Gly Val Ser Ala Leu Gly Val Thr Leu
 35 40 45
 Phe Gly Cys Pro Thr Met Lys Ser Pro Gly Gly Gly Asn Ala Thr Ile
 50 55 60
 Asn Pro Val Ala
 65

<210> 270
 <211> 552
 <212> DNA
 <213> SHRIMP

<400> 270
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 acatgtgtat gctcagttta ttcataatttt tccccttgct ggaaacatat aaaattttcc 120
 acatcgcatt cgcattgagg tataaaaaatc catcctccat caatattgaa ccataataact 180
 tctcttccca ccagtggaaa gatgtgtaac caccaccaca agagattgta cctgagcact 240
 gacgaccata cgagatggta tgacaaaaat acatcatgca tctatcttga agatattgga 300
 ggagtacaat tcatgggtata cgagttccat ctaacaccaa agaacaatca actattctcc 360
 ttccctgttc acctccaaat acacaacagg aatactgaga aaacatccct cctcgtattt 420
 gaaaatgaag aagatatgag ggtcaggaac attcatccaa aatccaagat attgatcccc 480
 gtgtccaaag acacagtgtc tgtagagaat gggtttcggt acaagggtgaa aattgtatta 540
 tcaaacaaat aa 552

<210> 271
 <211> 183
 <212> PRT
 <213> SHRIMP

<400> 271
 Met Phe Gln Lys Trp Phe Glu Ser Phe Leu Asp Ser Ser Arg Pro Arg
 1 5 10 15
 Tyr Leu Asp Thr Thr Cys Val Cys Ser Val Tyr Ser Tyr Phe Ser Pro
 20 25 30
 Cys Arg Lys His Ile Lys Phe Ser Thr Ser His Ser His Glu Gly Ile
 35 40 45
 Lys Ile His Pro Pro Ser Ile Leu Asn His Asn Thr Ser Ser Pro Thr
 50 55 60

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Ser Gly Lys Met Cys Asn His His His Lys Arg Leu Tyr Leu Ser Thr
 65 70 75 80
 Asp Asp His Thr Arg Trp Tyr Asp Lys Asn Thr Ser Cys Ile Tyr Leu
 85 90 95
 Glu Asp Ile Gly Gly Val Gln Phe Met Val Tyr Glu Phe His Leu Thr
 100 105 110
 Pro Lys Asn Asn Gln Leu Phe Ser Phe Pro Val His Leu Gln Ile His
 115 120 125
 Asn Arg Asn Thr Glu Lys Thr Ser Leu Leu Val Phe Glu Asn Glu Glu
 130 135 140
 Asp Met Arg Val Arg Asn Ile His Pro Lys Ser Lys Ile Leu Ile Pro
 145 150 155 160
 Val Ser Lys Asp Thr Val Leu Val Glu Asn Gly Phe Arg Tyr Lys Val
 165 170 175
 Lys Ile Val Leu Ser Asn Lys
 180

<210> 272
 <211> 684
 <212> DNA
 <213> SHRIMP

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 aacgcggaca gcatgttcat gcaaaccatg ctctcccta ccgacgccat gttcaccgat 120
 tgcgagtctc cattgtacaa gaacaagtcg ggaggggaaga atattgtcac cgatgttgga 180
 gagagtgtac tgtcttcttc ttcggacgaa aagatgagct tcaaagtgtc gtcccacgta 240
 ctccaggcgat tccctgtcct acttcattgc aactacaagc agacgaatac gcccctgtgg 300
 aaggagcttt acaagcacgg gaagtttgcc ctctcggcg acctggtgtt attctccaac 360
 ccattccacc ccaatatccc cgccatgccg ttgataaat ccccatattg tgacaccact 420
 ggaaaatcta tcattatgag tgaagtcatg accaaggagc tttgtacaa gttggccgac 480
 aaagatatgg gccatttctt tgctgtattg aatgtaacta accccattac tggagattct 540
 ttctccatt actttgcagg aggaaatacc atgagggatg gggaagggga taaaatctgc 600
 acatctgctg atgtgttacg cattattgct gagataacaa tacagaaaac tggcaagatg 660
 ccatatgaat tgatgaagaa ataa 684

<210> 273
 <211> 227
 <212> PRT
 <213> SHRIMP

<400> 273
 Met Asp Ser Leu Ile Ser Lys Leu Glu Asn Ile Phe Ser Ile Ala Glu
 1 5 10 15
 Gln Asp Phe Phe Asn Ala Asp Ser Met Phe Met Gln Thr Met Leu Leu
 20 25 30
 Pro Thr Asp Ala Met Phe Thr Asp Cys Glu Ser Pro Leu Tyr Lys Asn
 35 40 45
 Lys Ser Gly Gly Lys Asn Ile Val Thr Asp Val Gly Glu Ser Val Leu
 50 55 60
 Ser Ser Ser Ser Asp Glu Lys Met Ser Phe Lys Val Leu Ser His Val
 65 70 75 80
 Leu Arg Arg Phe Pro Val Leu Leu His Cys Asn Tyr Lys Gln Thr Asn
 85 90 95
 Thr Pro Leu Trp Lys Glu Leu Tyr Lys His Gly Lys Phe Ala Leu Leu
 100 105 110
 Gly Asp Leu Val Leu Phe Ser Asn Pro Phe His Pro Asn Ile Pro Ala
 115 120 125
 Met Pro Phe Asp Lys Ser Pro Ile Cys Asp Thr Thr Gly Lys Ser Ile
 130 135 140

Ile Met Ser Glu Val Met Thr Lys Glu Leu Leu Tyr Lys Leu Ala Asp
 145 150 155 160
 Lys Asp Ile Gly Gln Phe Phe Ala Val Leu Asn Val Thr Asn Pro Ile
 165 170 175
 Thr Gly Asp Ser Phe Leu His Tyr Phe Ala Gly Gly Asn Thr Met Arg
 180 185 190
 Asp Gly Glu Gly Asp Lys Ile Cys Thr Ser Ala Asp Val Leu Arg Ile
 195 200 205
 Ile Ala Glu Ile Thr Ile Gln Lys Thr Gly Lys Met Pro Tyr Glu Leu
 210 215 220
 Met Lys Lys
 225

<210> 274
 <211> 2193
 <212> DNA
 <213> SHRIMP

<400> 274
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 tcgaaaacgc caggagaagg agaaggagga gaaggaggag ggcaattcaa gataccttca 120
 gccatagctg tgaaatcttg ttgctctaaa aacgctactc gccgatcccc tccctcagat 180
 tctccttatt ctcttaggcc catgaagaga ctaaagaaga ataatggaga ggtgggagga 240
 aaagcaccgc ctcttgtagc tttgaggctc cgcgaggact acgagagcac accttacaac 300
 tttaatagaa ataagaagaa gaggcctatt actattgatg aaaatcaatt tgcaacatta 360
 aatccaacgt atgcgacaga cattatcaag aagcagcaat tgccttctgt tagtgccgcg 420
 tctgtgttga ggaagcaccg cgccaatgcc gacaccagc acagaaaaag attctctcat 480
 ccaaattgtg caaaattctc tactgtcaat ttgaaggcta gagactatac tccactgtct 540
 gtctctcggt cccatgtcaa ggggccaaaa cacttgaaat cttcttgtga taccgtgact 600
 gaaacaaatg tagtaaaagag gaacttttct tccattgaca agtgggtcaa gctagaaaaa 660
 ccccggtgtt actttgcagt ggcagaggct gataccaata ttgcagccgg tctagaatct 720
 ccgttccatt tgattagaca ggccgcaaaa ttaggcctca tttctgacgt gcaagatgtg 780
 tcgtccaact acgagaccat aaaacagagc tgtattgacg caaaggaaaa agcgtccaag 840
 tttttgtggt ctaacaaccg tactaaacaa ccccttcat cttggtggcc tgttgggttt 900
 ggtagtaaaa acctatccgt tttagacact agccctctct tgaactggaa caggttatgc 960
 aagaataatg gtaaaagggt gataaaaacc atgagcatcg atcacatggc aaagaatggt 1020
 ttttaagcttt cccctggagc atgtgaatct atattggaga agaaaaactac actcttgggg 1080
 gaggtcactg cccaatgtaa gaaatgggaa agttaccgca gaaatattcc tgtaccagca 1140
 cacgtccaac cagaatatgc ttctcaagtc gtaatgattg gaccatctga attatatctc 1200
 gaagttaaaq tcgggtgata ttacatgctt gaaactggaa aagttatcaa gtttatgacg 1260
 gacaaggaaa tgtactgtga atttgtattt gaaactgttt ttagtcacgc tcttgaggga 1320
 agaatagaag gcgcagtagg tgtgagaaag atgtgtgttg aaggtttttg tgtcgagatg 1380
 gattttgcag gcatttctgt gattgatgta ttaaatggag acctgaaatg taaaatggac 1440
 gagaatgttg tacagcaacc taaccctcgc actacttctt ccaagccagc cgctgagctc 1500
 atgcaagatc atggcagctt gtgtaggatg agggatactc tgtacggtgt taggatgctt 1560
 caagctactg gccgcctgcc tgaagggtcta caatctaaat gcaagaaacc cattacggat 1620
 tcaatttcag ccatagctat cggttgaaaa atgagggaga gaatgttaaa ccaattgccc 1680
 tttgttttgg tagaaattgt aaatattgtc actcgggtgt ctcaacaagg attagtgaat 1740
 cgggacataa aaagtgcaca tatagtaatt gatggaataa ctgggtcaacc taagatgatt 1800
 gatttttggt taattgtacc atgtaaaaag tactacaatt ttaaatgttg gggaaactgat 1860
 gagaggttct ttagtaacca tctcatata gctcctgaat ttattaacag tgagttgtgt 1920
 tcagaaactg ccatgacttt tgggttggtt tatttgttaa tagacatgtt gtccattttg 1980
 attaagagaa ctgcagattt gtctgccaat tctatctata caaacattcc atttttgtct 2040
 attgtatcta aaatgtatga ccaggaaaa accaataaggc cgagagcgta tgaaattgcg 2100
 cctgtaattg gtgcattgtt cccgttcaag gataatattg ctaaaactttt ccagtcacct 2160
 aaacattcat tgtatagcaa gaagggttaag tag 2193

<210> 275
 <211> 724
 <212> PRT

<213> SHRIMP

<400> 275

Met	Glu	Gly	Gly	Asp	Gln	Arg	Thr	Lys	Leu	Thr	Pro	Ala	Thr	Val	Met
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Gly	Gln	Ser	Lys	Thr	Pro	Gly	Glu	Gly	Glu	Gly	Gly	Glu	Gly	Gly	Gly
			20					25					30		
Gln	Phe	Lys	Ile	Pro	Ser	Ala	Ile	Ala	Val	Lys	Ser	Cys	Cys	Ser	Lys
		35					40					45			
Asn	Ala	Thr	Arg	Arg	Ser	Pro	Pro	Ser	Asp	Ser	Pro	Tyr	Ser	Leu	Arg
	50					55					60				
Pro	Met	Lys	Arg	Leu	Lys	Asn	Asn	Gly	Glu	Val	Gly	Gly	Lys	Ala	
65					70				75					80	
Pro	Pro	Pro	Val	Thr	Leu	Arg	Leu	Arg	Glu	Asp	Tyr	Glu	Ser	Thr	Pro
				85					90					95	
Tyr	Asn	Phe	Asn	Arg	Asn	Lys	Lys	Lys	Arg	Pro	Ile	Thr	Ile	Asp	Glu
			100					105					110		
Asn	Gln	Phe	Ala	Thr	Leu	Asn	Pro	Thr	Tyr	Ala	Thr	Asp	Ile	Ile	Lys
		115					120					125			
Lys	Gln	Gln	Leu	Pro	Ser	Val	Ser	Ala	Ala	Ser	Val	Leu	Arg	Lys	His
		130				135					140				
Arg	Ala	Asn	Ala	Asp	Thr	Gln	Tyr	Arg	Lys	Arg	Phe	Ser	His	Pro	Asn
145					150					155				160	
Cys	Ala	Lys	Phe	Ser	Thr	Val	Asn	Leu	Lys	Ala	Arg	Asp	Tyr	Thr	Pro
				165					170					175	
Leu	Ser	Val	Leu	Arg	Ser	His	Val	Lys	Gly	Pro	Lys	His	Leu	Lys	Ser
			180					185					190		
Ser	Cys	Asp	Thr	Val	Thr	Glu	Thr	Asn	Val	Val	Lys	Arg	Asn	Phe	Ser
		195					200					205			
Ser	Ile	Asp	Lys	Trp	Val	Lys	Leu	Glu	Lys	Pro	Pro	Cys	Tyr	Phe	Ala
	210					215					220				
Val	Ala	Glu	Ala	Asp	Thr	Asn	Ile	Ala	Ala	Gly	Leu	Glu	Ser	Pro	Phe
225					230					235					240
His	Leu	Ile	Arg	Gln	Ala	Ala	Lys	Leu	Gly	Leu	Ile	Ser	Asp	Val	Gln
				245					250					255	
Asp	Val	Ser	Ser	Asn	Tyr	Glu	Thr	Ile	Lys	Gln	Ser	Cys	Ile	Asp	Ala
			260					265					270		
Lys	Glu	Lys	Ala	Ser	Lys	Phe	Leu	Trp	Ser	Asn	Asn	Arg	Thr	Lys	Gln
		275					280					285			
Pro	Pro	Ser	Ser	Trp	Trp	Pro	Val	Gly	Phe	Gly	Ser	Lys	Asn	Leu	Ser
	290					295					300				
Val	Leu	Asp	Thr	Ser	Pro	Leu	Leu	Asn	Trp	Asn	Arg	Leu	Cys	Lys	Asn
305					310					315				320	
Asn	Gly	Lys	Gly	Trp	Ile	Lys	Thr	Met	Ser	Ile	Asp	His	Met	Ala	Lys
				325					330					335	
Asn	Val	Phe	Lys	Leu	Ser	Pro	Gly	Ala	Cys	Glu	Ser	Ile	Lys	Lys	Thr
			340					345					350		
Thr	Leu	Leu	Gly	Glu	Val	Thr	Ala	Gln	Cys	Lys	Lys	Trp	Glu	Ser	Tyr
			355				360					365			
Arg	Arg	Asn	Ile	Pro	Val	Pro	Ala	His	Val	Gln	Pro	Glu	Tyr	Ala	Ser
		370				375					380				
Gln	Val	Val	Met	Ile	Gly	Pro	Ser	Glu	Leu	Tyr	Leu	Glu	Val	Lys	Val
385					390					395				400	
Gly	Val	Tyr	Tyr	Met	Leu	Glu	Thr	Gly	Lys	Val	Ile	Lys	Phe	Met	Thr
				405					410					415	
Asp	Lys	Glu	Met	Tyr	Cys	Glu	Phe	Val	Phe	Glu	Thr	Val	Phe	Ser	His
			420					425					430		
Ala	Leu	Glu	Gly	Arg	Met	Lys	Gly	Ala	Val	Gly	Val	Arg	Lys	Met	Cys
		435					440					445			
Val	Glu	Gly	Phe	Cys	Val	Glu	Met	Asp	Phe	Ala	Gly	Ile	Ser	Val	Ile
	450					455					460				

Asp Val Leu Asn Gly Asp Leu Lys Cys Lys Met Asp Glu Asn Val Val
 465 470 475 480
 Gln Gln Pro Asn Pro Ser Thr Thr Ser Ser Lys Pro Ala Ala Glu Leu
 485 490 495
 Met Gln Asp His Gly Ser Leu Cys Arg Met Arg Asp Thr Leu Tyr Gly
 500 505 510
 Val Arg Met Leu Gln Ala Thr Gly Arg Leu Pro Glu Gly Leu Gln Ser
 515 520 525
 Lys Cys Lys Lys Pro Ile Thr Asp Ser Ile Ser Ala Ile Ala Ile Val
 530 535 540
 Gly Lys Met Arg Glu Arg Met Leu Asn Gln Leu Pro Phe Val Leu Val
 545 550 555 560
 Glu Ile Val Asn Ile Val Thr Arg Leu Ser Gln Gln Gly Leu Val Asn
 565 570 575
 Pro Asp Ile Lys Ser Asp Asn Ile Val Ile Asp Gly Ile Thr Gly Gln
 580 585 590
 Pro Lys Met Ile Asp Phe Gly Leu Ile Val Pro Cys Lys Lys Tyr Tyr
 595 600 605
 Asn Phe Lys Cys Trp Gly Thr Asp Glu Arg Phe Phe Ser Asn His Pro
 610 615 620
 His Thr Ala Pro Glu Phe Ile Asn Ser Glu Leu Cys Ser Glu Thr Ala
 625 630 635 640
 Met Thr Phe Gly Leu Ala Tyr Leu Leu Ile Asp Met Leu Ser Ile Leu
 645 650 655
 Ile Lys Arg Thr Ala Asp Leu Ser Ala Asn Ser Ile Tyr Thr Asn Ile
 660 665 670
 Pro Phe Leu Ser Ile Val Ser Lys Met Tyr Asp Gln Glu Lys Thr Asn
 675 680 685
 Arg Pro Arg Ala Tyr Glu Ile Ala Pro Val Ile Gly Ala Cys Phe Pro
 690 695 700
 Phe Lys Asp Asn Ile Ala Lys Leu Phe Gln Ser Pro Lys His Ser Lys
 705 710 715 720
 Lys Lys Val Lys

<210> 276
 <211> 615
 <212> DNA
 <213> SHRIMP

<400> 276
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 cttctagatg gaggtgcagc aatctgtctg cagtctaatt gtgttgcaag aaaacgtcac 120
 gccggttccc tccacgataa cctcttcaag atgctaggat ttggcgaccc ctataaacag 180
 agacggggaa aaacaaacag caaaaatctg gccataattg aagatagacc tcaactcggg 240
 tcagtatcag ttgtccaaca cccgacagaa ccagaaagggt tttgctccat gacattctta 300
 tttgctcagt acaatatggg taatggaaga aaatgttact tccctaacga caaagagtat 360
 gttgagagct gcaagaagca cgaaagggtc cacaaatctt ccacagaaat gaaaagattg 420
 cgcttgattt actttaacaa gtgtcttcac gcgatcgcca aatcacctgc aatgaagaag 480
 tacaacaaga taatcttccc tgccagaatt ggggtgcgcgg cagctggagg agattgggag 540
 aagtaccatg cttctattcg agatttctcc acaatcattg ataaggaagt gataatagtg 600
 tctcaaagga tgtaa 615

<210> 277
 <211> 204
 <212> PRT
 <213> SHRIMP

<400> 277
 Met Ser Ser Gly Lys Val Thr Tyr Glu Ile Val Glu Gly Gly Leu Leu

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Asn Asn Lys Tyr	Leu Leu Asp Gly	Gly Ala Ala Ile Cys	Leu Gln Ser
	20	25	30
Asn Cys Val Ala	Arg Lys Arg His	Ala Gly Ser Leu	His Asp Asn Leu
	35	40	45
Phe Lys Met Leu	Gly Phe Gly Asp	Pro Tyr Lys Gln	Arg Arg Gly Lys
	50	55	60
Thr Asn Ser Lys	Asn Leu Ala Ile	Ile Glu Asp Arg	Pro Gln Leu Gly
	65	70	75
Ser Val Ser Val	Val Gln His Pro	Thr Glu Pro Glu	Arg Phe Cys Ser
	85	90	95
Met Thr Phe Leu	Phe Ala Gln Tyr	Asn Met Gly Asn	Gly Arg Lys Cys
	100	105	110
Tyr Phe Pro Asn	Asp Lys Glu Tyr	Val Glu Ser Cys	Lys Lys His Glu
	115	120	125
Arg Val His Lys	Ser Ser Thr Glu	Met Lys Arg Leu	Arg Leu Tyr Tyr
	130	135	140
Phe Asn Lys Cys	Leu His Ala Ile	Ala Lys Ser Pro	Ala Met Lys Lys
	145	150	155
Tyr Asn Lys Ile	Ile Phe Pro Ala	Arg Ile Gly Cys	Ala Ala Ala Gly
	165	170	175
Gly Asp Trp Glu	Lys Tyr His Ala	Ser Ile Arg Asp	Phe Ser Thr Ile
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Ile Asp Lys Glu	Val Ile Ile Val	Ser Gln Arg Met	
	195	200	

<210> 278
 <211> 828
 <212> DNA
 <213> SHRIMP

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 ccagatattc ccgcaataac tgcaactact actactacta cagttgcaac acgtcacgac 720
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<210> 279
 <211> 275
 <212> PRT
 <213> SHRIMP

<400> 279
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 20 25 30
 Gln Gln Tyr Ser His Ser Phe Arg Pro Gln Gln Gln Gln His Gln
 35 40 45
 Lys Arg Thr Ser Thr Asn Ser Pro Pro Ala Pro Pro Pro Phe Pro

50		55		60
Ile Ile Ser Trp Gly Ala Leu Gly Ser Tyr Ser Met Tyr Arg Leu Asp				
65		70		75
Asp Gln Cys Arg Asn Cys Asp Glu Thr Gly Tyr Tyr Asn Phe His Ser				
	85		90	
Tyr Asp Arg Lys Arg Glu Arg Val Arg Ser Leu Asn Asn Thr Pro Ser				
	100		105	
Glu Gly Met Trp Arg Arg Thr Ser Arg Ser Ser Pro Phe Leu Asn Lys				
	115		120	
Lys Lys Asp Val Asp Glu Ala Pro Pro Pro Gln Ser Asn Gln His Met				
	130		135	
Tyr Pro Leu Asn Lys Tyr Ser Phe Arg Glu Tyr Thr Pro Ser Ser Lys				
	145		150	
Leu Val Asn Trp Arg Asp Pro Ser Gln Glu Lys Gln Asp Lys Ile Leu				
	165		170	
Gln Glu Glu Glu Ala Arg Ala Pro Thr Pro Thr Pro Gln Glu Lys Glu				
	180		185	
Pro Glu Val Glu Thr Lys Asp Asp Val Val Ile Glu Glu Glu Thr Ala				
	195		200	
Pro Glu Pro Glu Pro Glu Pro Ala Pro Val Pro Asp Pro Asp Ile Pro				
	210		215	
Ala Ile Thr Ala Thr Thr Thr Thr Thr Thr Val Ala Thr Arg His Asp				
	225		230	
Asp Ser Ser Thr Val Phe Leu Arg Asn Val Ile Leu Ser Ile Val Phe				
	245		250	
Trp Phe Leu Gly Val Tyr Ser Ala Leu Phe Ala Lys Cys Ile Arg Ser				
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Lys Lys Glu				
	275			

<210> 280
 <211> 2025
 <212> DNA
 <213> SHRIMP

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 aacttaaaat tgggcgattc tcttaaagaa actgatgtta atttgggaata cttgagatac 180
 gcgtctacgc ccctccttgg ggaattaaac tacgacaaac aacaatatgc ggcaacagtt 240
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gagcaagaag cagcactatc tacagaacac tgtatttggt taacgatttt gtggaaacaa 1980
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<210> 281

<211> 672

<212> PRT

<213> SHRIMP

<400> 281

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Asp Ala Leu Met Thr Arg Leu Ala Asn Leu Lys Leu Gly Asp Ser Leu
35     40     45
Lys Glu Thr Asp Val Asn Leu Glu Tyr Leu Arg Tyr Ala Ser Thr Pro
50     55     60
Leu Leu Gly Glu Leu Asn Tyr Asp Lys Gln Gln Tyr Ala Ala Thr Val
65     70     75     80
Asp Ile Asn Leu Met Ala His Phe Ser Tyr Ala Ala Leu Gly Ile Glu
85     90     95
Ser Ile Leu Asn Ser Ile Arg Arg Val Val Ala Asn His Gln Arg
100    105    110
Arg Asn Asn Gly Lys Lys Pro Ser Glu Pro Ile Ser Arg Pro His Pro
115    120    125
Leu Gly Gly Val Glu Pro Pro Leu Ser Ser Glu Leu Ala Asn Ala Ile
130    135    140
Arg Asp Lys Phe Ile Ser Met Gly Ala Leu Asp Arg Leu Asn Ser Ala
145    150    155    160
Ile Val Thr Ala Ala Leu Gly Ala Ile Ala Ser Glu Leu Phe Leu Arg
165    170    175
Glu Asn Ala Val Asn Tyr Met Tyr Asp Val Glu Phe Ala Glu Arg Asp
180    185    190
Ala Ala Thr Thr Asp Thr Gly Asn Val Val Tyr Leu Ser Thr Lys Met
195    200    205
Asp Glu Asp Glu Asp Asp Ile Ile Lys Arg Ser Glu Ile Leu Asp Lys
210    215    220
Val Ser Lys Arg Pro Ala Lys Glu Gly Ile Asp Trp Arg Pro Thr Pro
225    230    235    240
Asp Asn Ser Phe Pro Tyr Gln Leu Ile Trp Gly Asp Asp Ser Val Asp
245    250    255
Asp Thr Val Leu Ile Asp Leu Ile Thr Asn Ala Ile Val Pro Asn Ile
260    265    270
Phe Met Ala Lys Phe Ile Leu Phe Ile Cys Asn His Leu Arg Ala Val
275    280    285
Ile Arg Ser Met Arg Glu Ile Leu Tyr Gly Asn Ile Ser Ser Ser Ser
290    295    300
Asp Asn Tyr Phe Glu Asp Gly Arg Lys Trp Cys Phe Trp Leu Asn Leu
305    310    315    320
Tyr Asn Arg Leu Glu Trp Phe Met Leu Val Val Arg Phe Val Ile Phe
325    330    335
Leu His Ser Lys Lys Glu Ser Phe Ser Gly Ala Asp Asn Val Asn Val
340    345    350

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Lys Arg Leu Leu Val Val Val Val Glu Ser Phe Pro Pro Val Leu Leu
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 Asp Thr Glu Trp Val Lys Thr Asn Ile Thr Ser Trp Pro Val Ile Asn
 370 375 380
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 385 390 395 400
 Arg Leu Ala Ile Arg Thr Ser Ser Gly Ala Arg His Pro Ile Phe Asp
 405 410 415
 Glu Ile Asn Ser Leu Thr Thr Ala Val Thr Asn Arg Ile Thr Phe Gln
 420 425 430
 Ser Ala Glu Phe Cys Thr Lys Ile Leu Leu Gly Arg Ala Leu Asp Glu
 435 440 445
 Glu Glu Ala Gly Thr Lys Met Leu Val Lys Ser Val Lys Glu Thr Gly
 450 455 460
 Glu Glu Lys Asp Lys Asn Asn Thr Phe Ser Ser Phe Gly Leu Leu Leu
 465 470 475 480
 Lys Asn Thr Lys Asn Glu Glu Leu Glu Ile Asn Ile Gly Asp Asn Asp
 485 490 495
 Asp Glu Thr Thr Asp Val Ala Cys Trp Ala Arg Thr Ser Ser Thr Ser
 500 505 510
 Phe Ile Arg Asn Arg Thr Tyr Ala Phe Lys Lys Ile Trp Gly Leu Glu
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 Ser Phe Val Thr Asp Lys Ser Ser Pro Leu Leu Phe Pro Tyr Val Ser
 545 550 555 560
 Asp Trp Ser Cys Leu Leu Leu His Pro Cys Cys Lys Ala Pro Ala Ile
 565 570 575
 Ile Lys Ser Val Trp Leu Gln Ile Leu Lys Asp Phe Ser Gln Glu Asn
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 Ile Lys Thr Ile Asn Glu Lys Val Gln Ser Leu Ser Ser Glu Ile Cys
 595 600 605
 Gln Lys Ser Asn Asp Arg Phe Lys Asn Lys Lys Ile Ala Ala Glu His
 610 615 620
 Val Arg Ser Val Lys Lys Leu Leu Asn Thr Ile Ser Asn Arg Glu Gln
 625 630 635 640
 Glu Ala Ala Leu Ser Thr Glu His Cys Ile Trp Leu Thr Ile Leu Trp
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<210> 282

<211> 2535

<212> DNA

<213> SHRIMP

<400> 282

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 aatccggaat catccatata tagaactccg atatccctct tccaaaacaa ggatattggt 180
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<210> 283

<211> 838

<212> PRT

<213> SHRIMP

<400> 283

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Pro Glu Phe Glu Glu Asp Val Lys Asn Pro Glu Ser Ser Ile Tyr Arg
 35          40          45
Thr Pro Ile Ser Leu Phe Gln Asn Lys Asp Ile Val Thr Ile Val Gly
 50          55          60
Asp Tyr Ile Leu Ser Pro Lys Thr Asp Ser Phe Gln Val Leu Tyr Pro
 65          70          75          80
Ile Lys Lys Val Ile Glu His Phe Pro Val Ile Phe His Cys Thr His
 85          90          95
Asn Asn Ala Pro Leu Trp Val His Leu Leu Asp Glu Arg His His Arg
 100          105          110
Leu Leu Gln Ser Leu Leu Thr Tyr Glu Ile Val Asn Ala Lys Tyr Arg
 115          120          125
Gly Ile Val Val Ile Pro Tyr Tyr Arg Arg Pro Ile Asn Tyr Gln Thr
 130          135          140
Gly Lys Ser Leu Leu Met Ser Lys Leu Ala Ser Val Lys Val Leu Asp
 145          150          155          160
Ile Leu Met Arg Cys Gly Ser Tyr Lys Phe Ile Ser Leu Met Cys Met
 165          170          175
Ile Asn Lys Lys Asn Asn Thr Asn Phe Leu His Cys Cys Ala Ser Lys
 180          185          190

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Ala	Ile	Gln	Glu	Asp	Asn	Ala	Asp	Ala	Leu	Leu	Phe	Leu	Ile	Ser	Leu
				245					250					255	
Tyr	Gly	Ala	Pro	Trp	Phe	Gln	Asp	Asn	Asn	Ser	Tyr	Met	Lys	Ser	Ala
			260					265					270		
Leu	Glu	Leu	Lys	Ser	Asn	Lys	Cys	Val	Lys	Val	Leu	Ser	Phe	Ala	Ala
	275						280					285			
Asp	Lys	Tyr	Glu	Ile	Leu	Pro	Asn	Ile	Asn	Asn	Asn	Gln	Leu	Glu	Pro
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Glu	Gly	Lys	Thr	Thr	Ser	Leu	Ser	Trp	Tyr	Gln	Met	Asn	Cys	Lys	His
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Tyr	Ile	His	Cys	Glu	Cys	Leu	Met	Gly	Met	Cys	Ala	Ala	Ala	Gly	Asn
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Val	Gln	Cys	Pro	Met	Cys	Arg	Glu	Asp	Val	Gly	Asp	Glu	Val	Leu	Glu
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Gln	Met	Glu	Ala	Met	Lys	Pro	Pro	Arg	Val	Val	Val	Pro	Pro	Arg	Arg
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Thr	Phe	Leu	Thr	Pro	Ala	Arg	Arg	Gly	Glu	Arg	Ala	Ile	Arg	Ile	Ala
			420					425					430		
Arg	Glu	Ile	Ala	Thr	Asn	Ala	Ile	Ala	Glu	Ala	Thr	Ala	Gln	Gly	Asp
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	450					455					460				
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Arg	Pro	Phe	Leu	Glu	Asp	Glu	Glu	Glu	Ala	Arg	Gln	Ile	Gln	Met	Arg
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Gln	Phe	Ala	Glu	Leu	Ser	Arg	Arg	Gly	Val	Ser	Val	Asn	Ile	Ile	Asn
			500					505					510		
Asn	Asp	Asn	Pro	His	Arg	His	Thr	Val	Asn	Ile	Val	Gln	Pro	Val	Tyr
		515					520					525			
Gly	Val	Glu	Lys	Ser	Pro	Ala	Ala	Ser	Phe	Ile	Tyr	Asn	Met	Leu	Lys
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Asn	Asp	Val	Phe	Glu	Ser	Ile	Arg	Ser	Arg	Asp	Thr	Arg	Val	Gly	Gly
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Glu	Arg	Val	Pro	Val	Met	Asn	Leu	Ser	Asn	Asp	Lys	Arg	Ala	Leu	Phe
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His	Ala	Ala	Ser	Ser	Met	Leu	Cys	Asp	Phe	Ala	Thr	Glu	Thr	Asn	Ser
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Gln	Ile	Val	Gly	Leu	Asp	Phe	Gln	Ala	Val	Tyr	Asp	Pro	His	His	Asn
		595					600					605			
Tyr	Ile	Glu	Thr	Phe	Gly	Ser	Pro	Leu	His	Ala	Tyr	Pro	Gly	Ala	Val
	610					615					620				
Thr	Phe	Leu	Asp	Gly	Ala	Gln	Asp	Tyr	Tyr	Ala	Glu	Ser	Ile	Arg	Tyr
625					630					635					640
Asp	Asn	Asp	Ile	Val	Ser	Phe	Ser	Glu	Met	Ala	Ser	Glu	Leu	His	Ile
				645					650					655	
Thr	Glu	Ala	Leu	Asp	Val	Phe	Glu	Gly	Ser	Leu	Leu	Ser	Pro	Leu	Phe
			660					665					670		
Lys	Lys	Ile	Arg	Thr	Gly	Lys	Ser	Tyr	Ser	Asn	Trp	Asn	Asp	His	Leu

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690	695	700
Cys Glu Asn Ser Leu Ala Ser Arg Glu His Pro Pro Val His Val His		
705	710	715
Pro Phe Arg Asp Gly Ala Ile Pro Ile Leu Ile Glu Tyr Ile Val Asp		
	725	730
Phe Ile His His Cys Ile Thr Trp Ser Met Gln Val Asn Ala Leu His		
	740	745
Cys Met Arg Lys Tyr Ile Glu His Glu Asn Thr Asn Val His Leu Leu		
	755	760
Asn Leu Arg Pro Thr Asp Glu Arg Val Glu Val Leu Arg Val Ser Gln		
	770	775
Leu Arg Trp Ser Arg Leu Phe Asn Glu Gln Tyr Asn Thr Arg Met Ser		
785	790	795
Leu Ser Thr Lys Arg Leu Ser Leu Met Lys Ile Phe Asn His Asp Leu		
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Gly Val Ser Lys Phe Gly Val Tyr Lys Leu Leu Asp Ile Ile Glu Met		
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Tyr Cys Phe Thr Leu Ile		830
835		

<210> 284

<211> 2799

<212> DNA

<213> SHRIMP

<400> 284

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<210> 285

<211> 924

<212> PRT

<213> SHRIMP

<400> 285

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 20          25          30
Lys Thr Gly Ile Cys Glu Glu Ala Ala Ala Asn Gly Arg Pro Tyr Leu
 35          40          45
Pro Thr Leu Glu Met Arg Asn Glu Val Asp His Phe Trp Ser Gln Asp
 50          55          60
Asn Arg Lys Leu Lys Leu Leu Gly His Phe Cys Gly Asn Leu Tyr Val
 65          70          75          80
Glu Ala Phe Ile Ala Gly Ser Ile Asp Ala Glu Thr Cys Val Gly Phe
 85          90          95
Leu Arg Ser Gln Ala Thr Gly Leu Gly Tyr Pro Leu Leu Lys Lys Leu
100          105          110
Ala Leu Ile Ala Arg Glu Asp Lys Ser Asn Thr Thr Asn Tyr Asn Leu
115          120          125
Tyr Ile Asp Arg Asn Ser Met Met Lys Gln Val Phe Ser Ala Glu Ile
130          135          140
Asp Lys Arg Pro Ser Ser Ile Gln Asn Thr Ser His Thr Lys Ser Ser
145          150          155          160
Pro Val Tyr Leu Lys Leu Ile Asp Arg Arg Thr Glu Cys Leu Ala Leu
165          170          175          180
Asp Trp Leu Asp Ala Ser Lys Arg Thr Ala Lys Glu Ile Gly Ala Ala
180          185          190
Arg Lys Val Cys Phe Leu Gln Asn Leu Ile Val Ala Ile Leu Ile Pro
195          200          205
Ala Tyr Thr Glu Thr Phe Val Leu Asp Thr Gly Asn Glu Leu Glu Gln
210          215          220
Gln Val Leu Asp Asp Ala Tyr Phe Asn Ala Glu Asn Lys Asp Lys Val
225          230          235          240
Asp Glu Met Cys Val Val Ala Ile Leu Ser Thr Leu His Asn Leu Phe
245          250          255
Val Arg Lys Ser Leu Pro His His Leu Tyr Asn Ala Pro Phe Arg Leu
260          265          270
Pro Pro Phe Gly Gln His Pro Ile Ile Asn Ile Glu Asn Ser Ser Phe
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Phe Asn Glu Asp Thr Thr Pro Ile Leu Ala Ser Ile Ser Ile Pro Ser
290          295          300
Ser Met Val Ile Lys His His Thr Arg Lys Asn Ser Arg Trp Arg Cys

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Pro	Asn	Asn	Leu	Met	Thr	Ala	Ala	Glu	Arg	Ser	Ile	Phe	Leu	Arg Gly
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Ser	Thr	Ile	Met	Pro	Ser	Val	Leu	Phe	Tyr	Gly	Asp	Arg	Lys	His Leu
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Ile	Asn	Thr	Val	Lys	Ser	Asn	Asn	Phe	Ser	Ala	Ile	Thr	Cys	Ser Tyr
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Trp	Asn	Lys	Tyr	Met	Asp	Cys	Arg	Ser	Tyr	Gly	Phe	Glu	Ile	Ile Asp
385					390					395				400
Thr	Pro	Glu	Asn	Asn	Cys	Gly	Phe	Arg	Ile	Arg	Ala	Ala	Ile	Asp Cys
			405						410					415
Ser	Asn	Thr	Asp	Phe	His	Ser	Pro	Val	Thr	Arg	Val	Asn	Lys	Lys Lys
		420						425					430	
Thr	Ser	Ile	Ile	Asn	Ala	Val	Lys	Asn	Pro	Phe	Phe	Ile	Arg	His Thr
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Met	Asp	Arg	Phe	Gly	Ser	Leu	Leu	Leu	Gly	Arg	Glu	Lys	Lys	Trp Thr
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Cys	Asn	Tyr	Leu	Asp	Arg	Ile	Lys	Ser	Leu	Glu	Thr	Ile	Ser	Asn Asn
		500						505					510	
Leu	Lys	Gly	Lys	Ile	Asp	Thr	Met	Cys	Lys	Ile	Thr	Lys	Tyr	Asn Tyr
	515						520					525		
Lys	Ser	Ser	Ser	Leu	Tyr	Tyr	Lys	Gln	Ile	Thr	Ala	Thr	Ser	Asp Asp
	530					535					540			
Pro	Ile	Lys	Met	Lys	Ile	Ile	Ala	Ser	Ile	Asn	Lys	Arg	Arg	Tyr Leu
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Cys	Asn	Ile	Phe	Ala	Ile	Ile	Ser	Ser	Glu	Lys	Lys	Asp	Glu	Val Glu
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Glu	Asp	His	Thr	Lys	Thr	Gly	Asn	Gly	Gly	Cys	Ala	Phe	Ser	Lys Tyr
		580					585					590		
Lys	Lys	Lys	Gln	Leu	Glu	Pro	Lys	Gln	His	Leu	Ile	Val	Lys	Val Asn
	595					600						605		
Lys	Tyr	Ile	Glu	Ala	Phe	Ser	Leu	Ile	Lys	Met	Leu	Arg	Asn	Asp Cys
	610					615					620			
Glu	Arg	Asn	Lys	Cys	Arg	Phe	Lys	Glu	Ala	Glu	Ile	Arg	Glu	Cys Ala
625					630					635				640
Asn	Glu	Leu	Val	Arg	Glu	Leu	Tyr	Arg	Ala	Ser	Ala	Arg	Ser	Tyr Val
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His	Asp	Leu	Val	Leu	Lys	Arg	Thr	Asn	Val	His	Leu	Thr	Trp	Gln Arg
	660						665						670	
Pro	Tyr	Asp	Glu	Asn	Ala	Asn	Thr	Ile	Met	Ser	Leu	Ile	Pro	Lys Cys
	675						680					685		
Lys	Leu	His	Thr	Val	Leu	Tyr	Asp	Lys	Asp	Ser	Arg	Asp	Val	Lys Leu
	690					695					700			
Leu	Asn	Phe	Leu	Arg	Thr	Arg	Asp	Gly	Asn	Tyr	Asn	Pro	Ile	Arg His
705					710					715				720
Ser	Met	Leu	Glu	Leu	Val	Tyr	Gly	Glu	Glu	Tyr	Ala	Lys	Asp	Val Ser
			725						730					735
Thr	Val	Thr	Cys	Phe	Glu	Trp	Leu	Lys	Trp	Cys	Ser	Lys	Lys	Gly Val
		740						745					750	
Ile	Lys	Tyr	Glu	Asp	Phe	Leu	Asp	Arg	Tyr	Glu	Lys	Thr	Gly	Glu Glu
	755						760					765		
Asp	Lys	Asp	Glu	Arg	Glu	Phe	Phe	Arg	Leu	Lys	Lys	Cys	Ser	Arg Asp
	770					775					780			
His	Thr	Lys	Asp	Ile	Lys	Lys	Ile	Glu	Asn	Val	Leu	Asn	Ser	Asp Thr
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Lys Tyr Ser Leu Asp Lys Asn Val Gln Thr His Ala Ser Ser Ser Thr
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 Val Val Lys Asn Asp Thr Asp Gly Lys Thr Ser Met Val Gly Trp Asp
 820 825 830
 Tyr Ile Phe Ser Ile Gly Lys Gly Glu Lys Thr Thr Lys Lys Arg Lys
 835 840 845
 Leu Glu Thr Ile Asp Ile Ser Ser Ser Asp Asp Asp Glu Glu Glu
 850 855 860
 Glu Glu Glu Asp Glu Gly Lys Arg Met Lys Met Asn Asn Cys Ser Ser
 865 870 875 880
 Ser Ile Lys Asn Lys Ser Lys Asn Lys Asn Gly Arg Met Cys Cys Thr
 885 890 895
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 <213> SHRIMP

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 atagccatgg atggagatta tgcgacatta gtaaggaacg gaatgtccac aaatcaaagg 240
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 ccaaatccca ttacaattc tactgaaaag ccgtatatta acacggagat aacttccatc 480
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 <212> DNA
 <213> SHRIMP

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 aaaaaaaaaa a 431

<210> 288
 <211> 1103
 <212> DNA
 <213> SHRIMP

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<211> 234

<212> DNA

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<210> 290

<211> 597

<212> DNA

<213> SHRIMP

<400> 290

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aagaagaaaa agcaatgggt atcaatacag ataatggagg atttgttttg aagaatgggt 540
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<210> 291

<211> 335

<212> DNA

<213> SHRIMP

<400> 291

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ttcctcaaa agcggaagaa agtctggagc ccgcaagtca aggcgttaat tcttccctgt 240
acaacaacta tgttatttaa ttgatttttt ttcttctgaa taattggaaa taataaaaca 300
tccattgaaa cttaaaaaaa aaaaaaaaaa aaaaaa 335

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<210> 292

<211> 225

<212> DNA

<213> SHRIMP

<400> 292

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ttgaaaagtt ttgagatgg aggaagagta aaattcccta gtgtaaacag taccaagaag 180
accaataaat ttagtggtta taaaactaca catatgatta aaaaa 225

<210> 293

<211> 107

<212> DNA

<213> SHRIMP

<400> 293

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atgtacactc tgtaatttt ttcaaacaat aaactaacca ctttgta 107